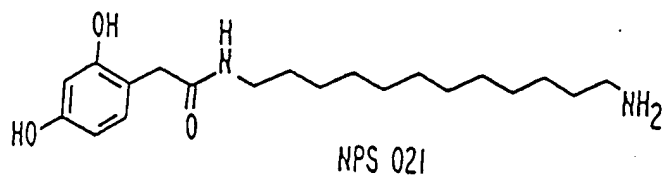
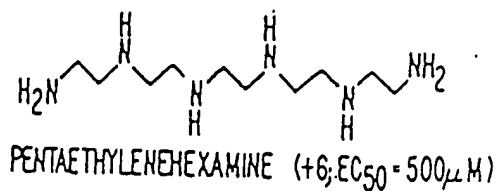
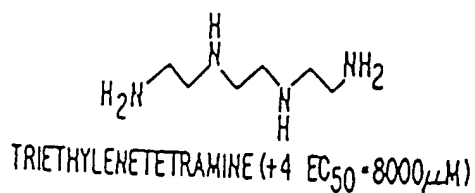
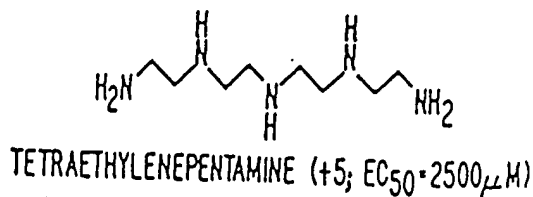
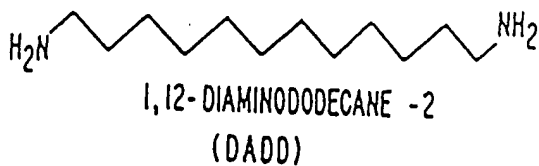
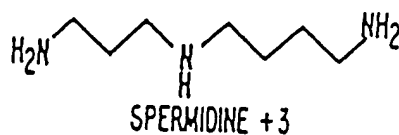
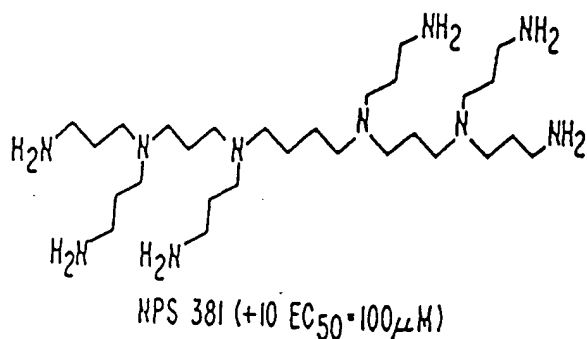
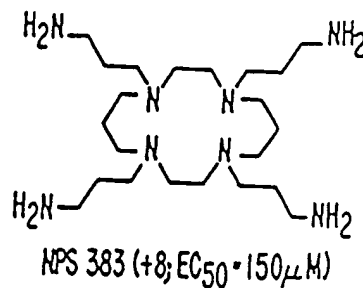
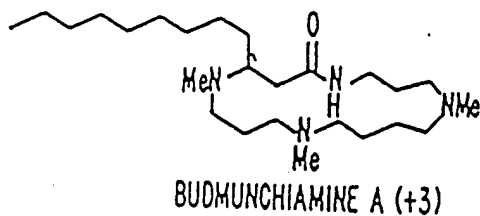
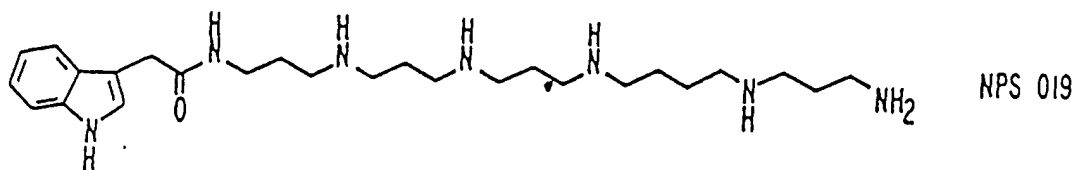
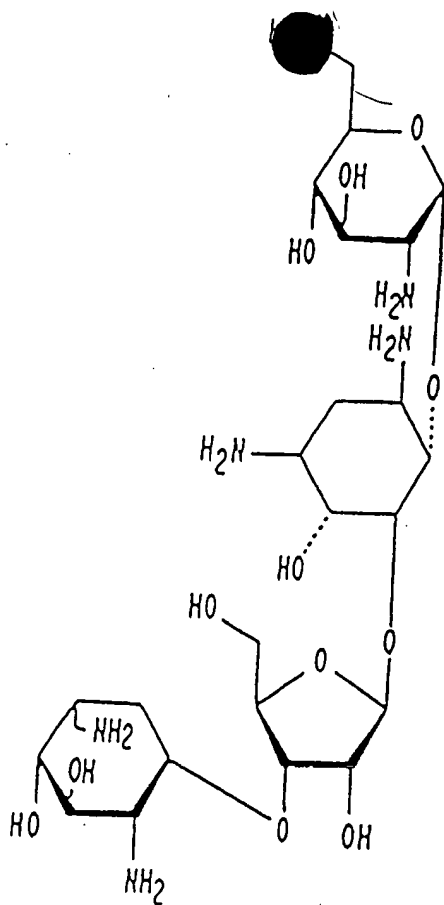
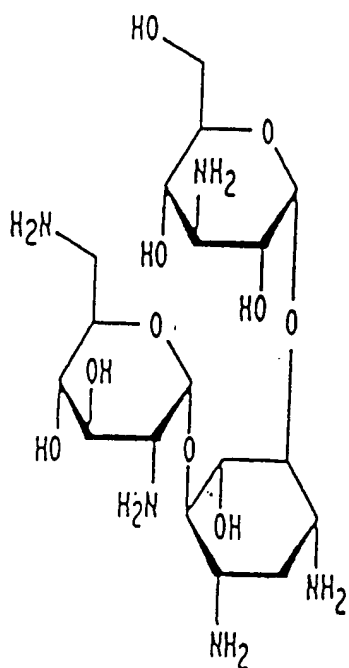


FIG. 1a.

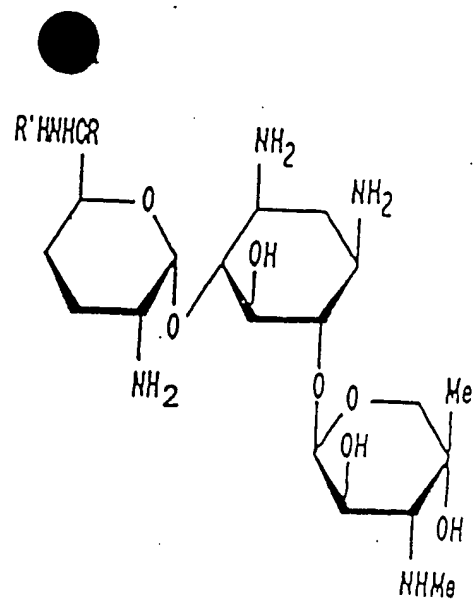




Neomycin B (+6)



Bekanamycin (+5)

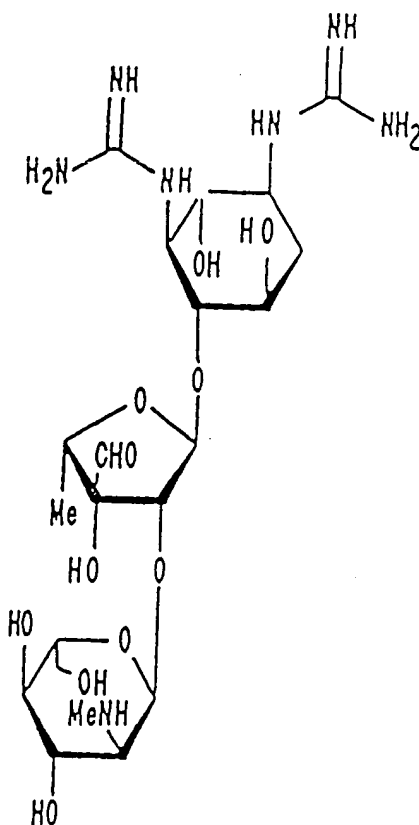


Gentamicin (Complex +5)

C1 R=R'=Me

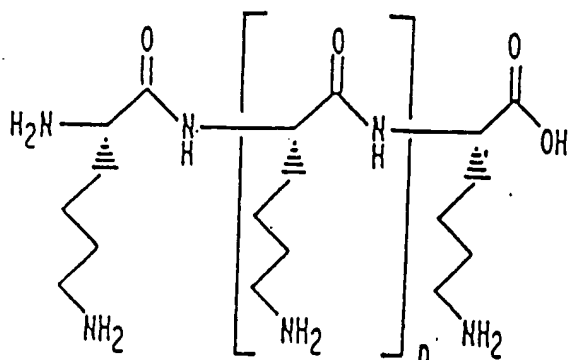
C2 R=Me; R'=H

C1aR=R'=H

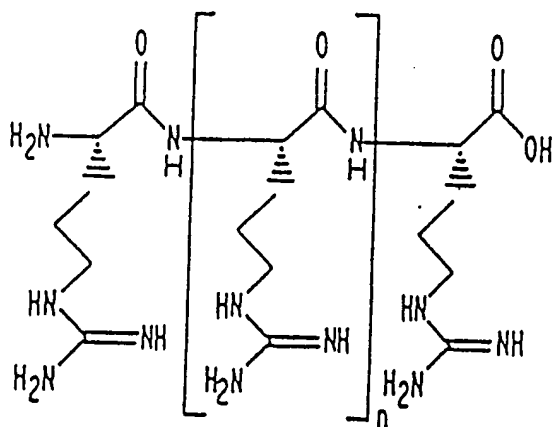


Streptomycin (+3)

FIG. 1b.



poly-Lys (27 kD) n = 210 + 210
 poly-Lys (14 kD) n = 110 + 110
 poly-Lys (38 kD) n = 55 + 55

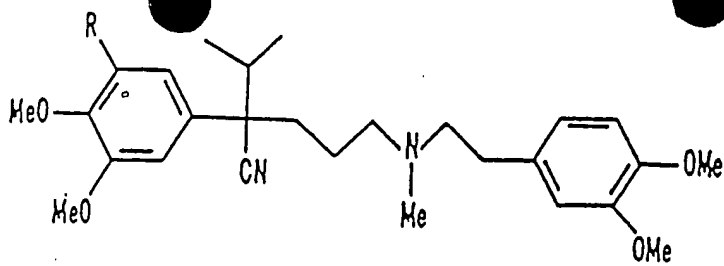


poly-Arg (100 kD) n = 640 + 640
 poly-Arg (40 kD) n = 256 + 256

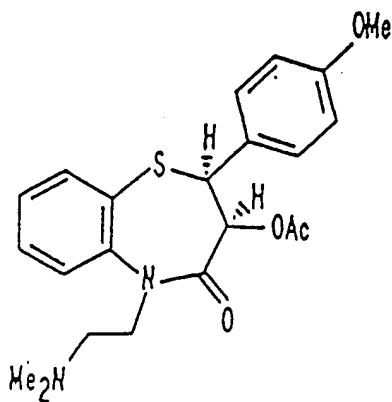
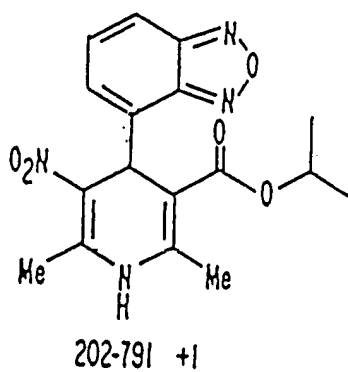
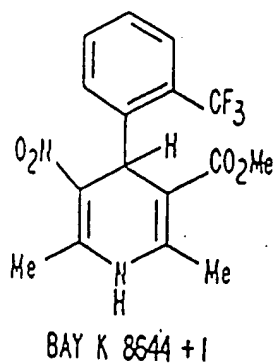
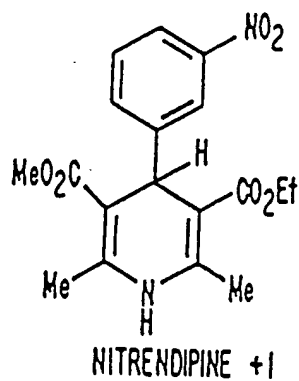
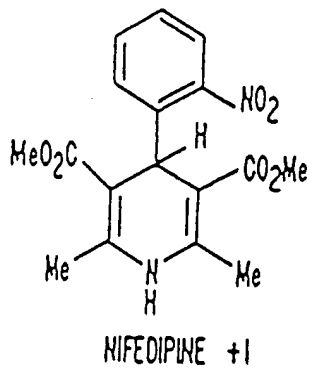
PROTAMINE +21

H₂N-Pro-Arg-Arg-Arg-Arg-Ser-Ser-Ser-Arg-Pro-Val-Arg-Arg-Arg-Arg-Arg-
 Pro-Arg-Val-Ser-Arg-Arg-Arg-Arg-Arg-Arg-Gly-Gly-Arg-Arg-Arg-OH

FIG. 1c.

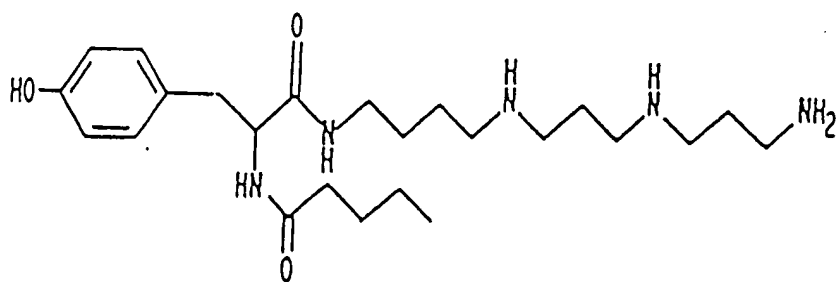


VERAPAMIL R=H +I
D-600 R=OMe +I

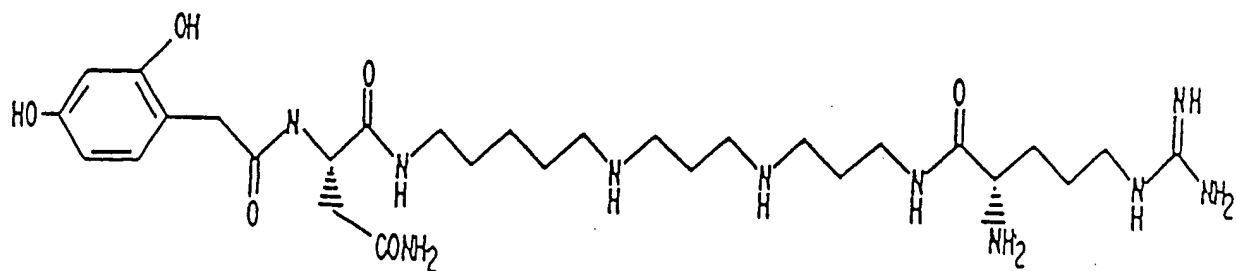


DILTIAZEM +I

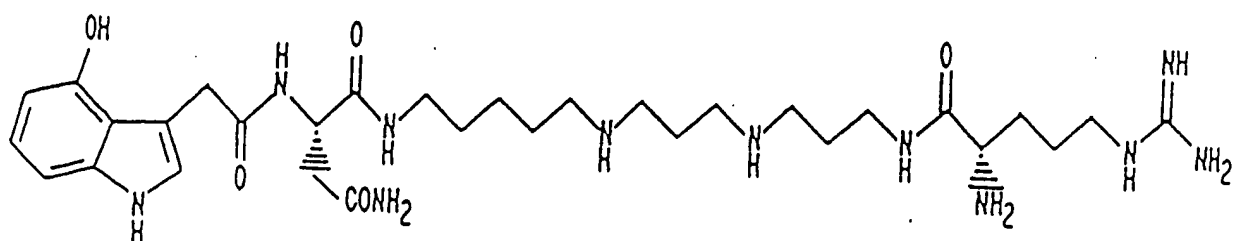
FIG. 1d.



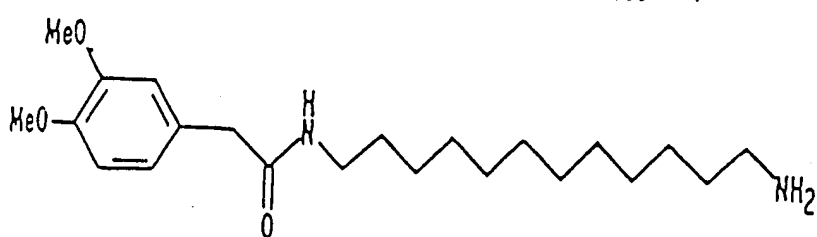
PHILANTHOTOXIN 433 +3



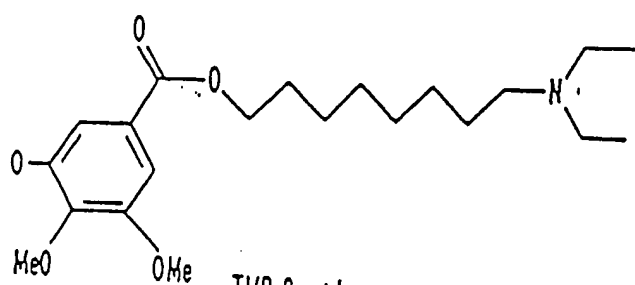
ARGIOTOXIN 636 +4



ARGIOTOXIN 659 +4



NPS 384 +1



TMB-8 +1

FIG. 1e.

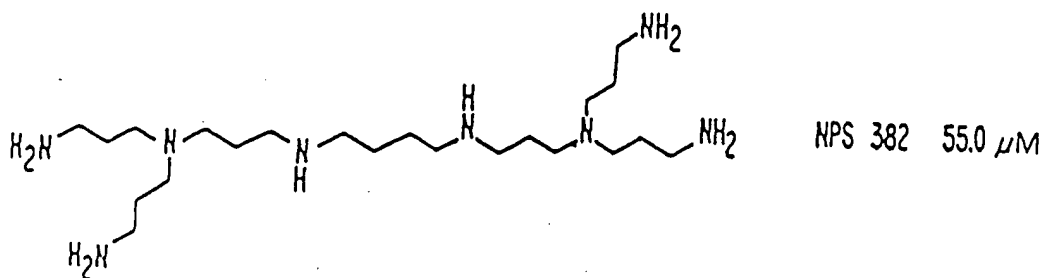
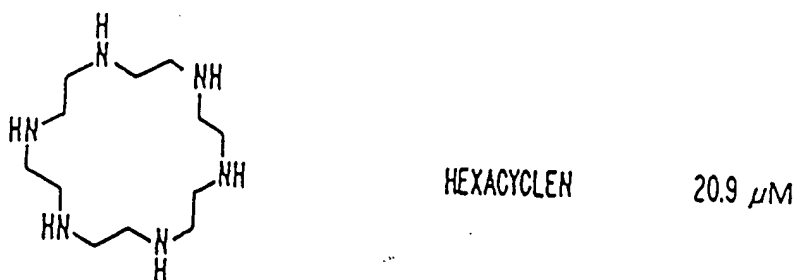
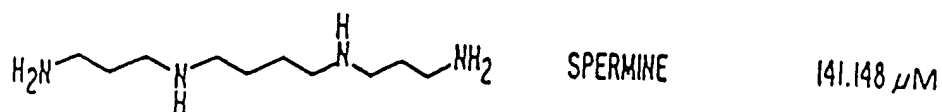
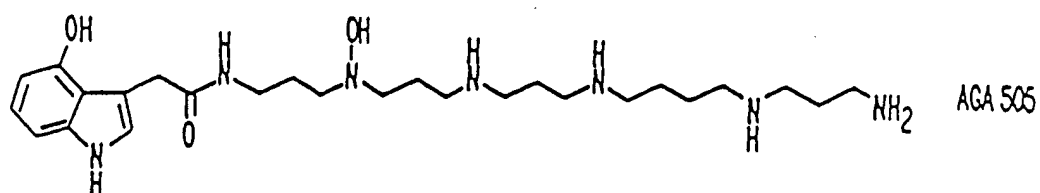
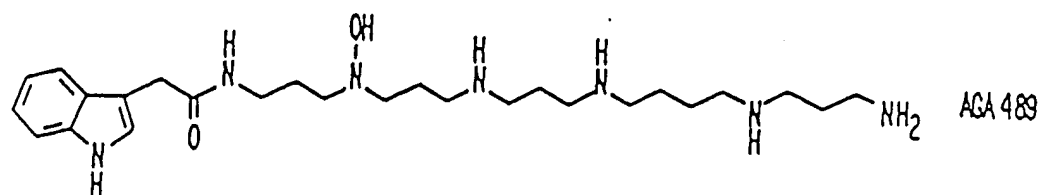


FIG. 1f.

FIG. 2.

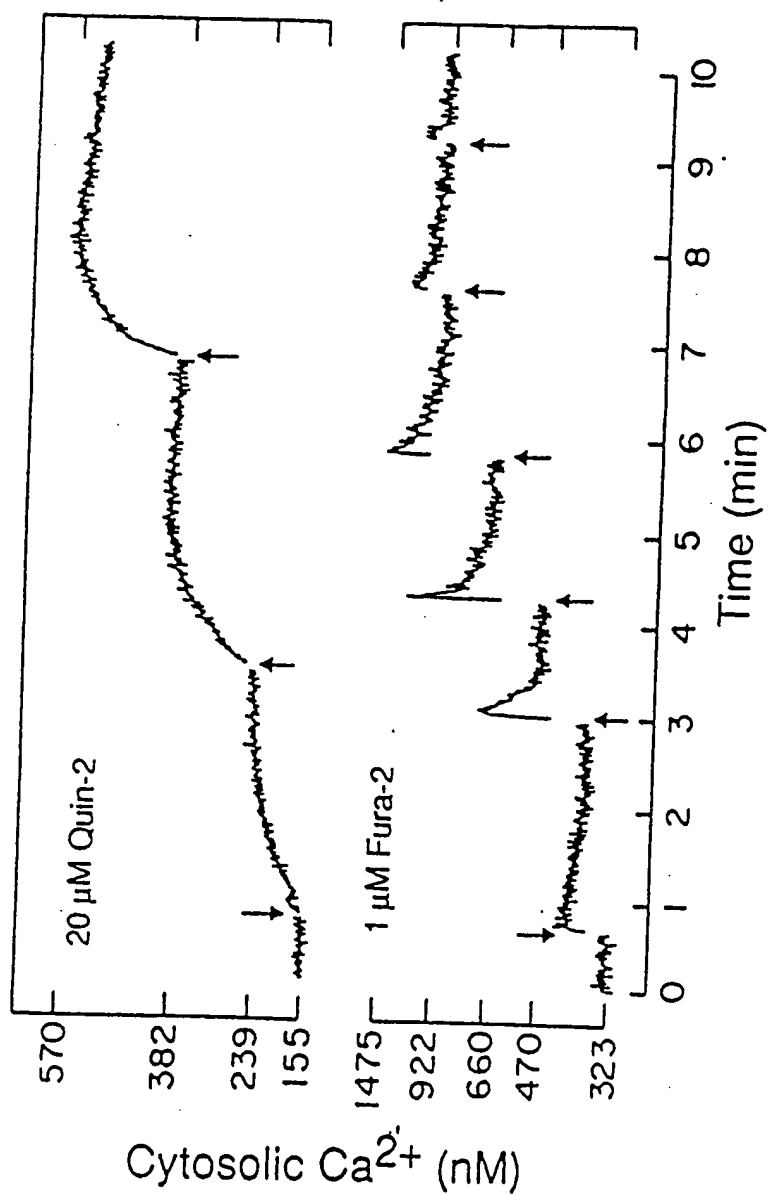


FIG. 3a.

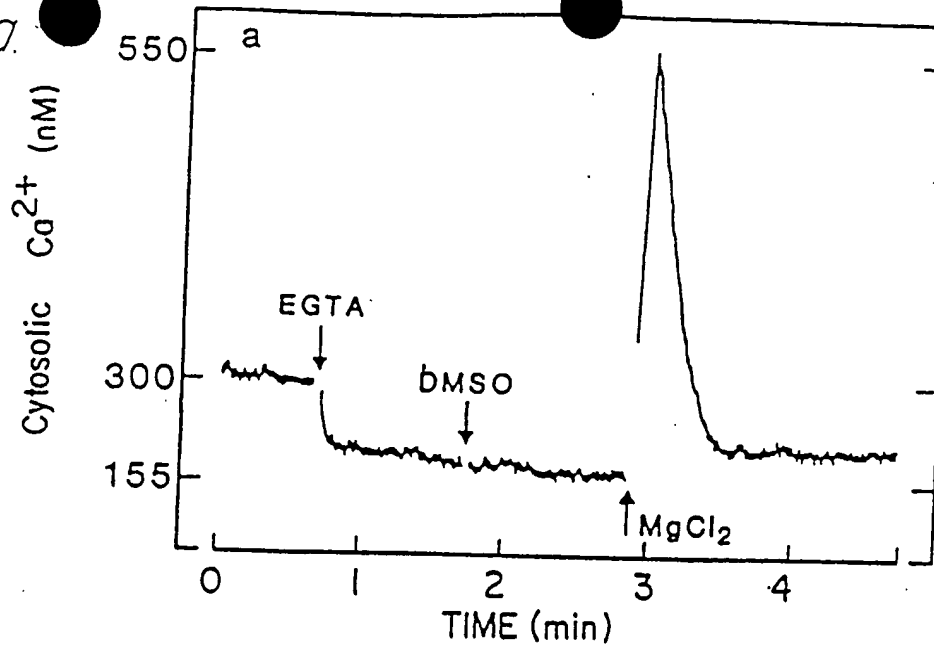


FIG. 3b.

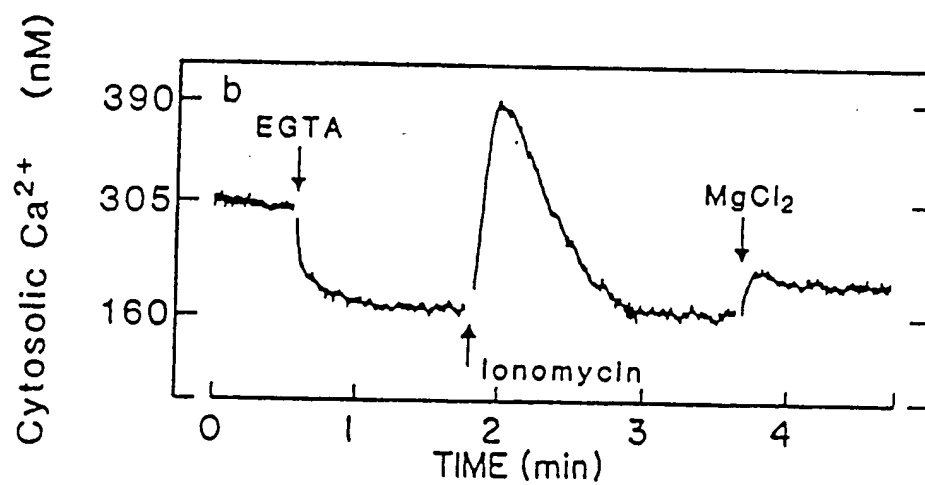


FIG. 3c.

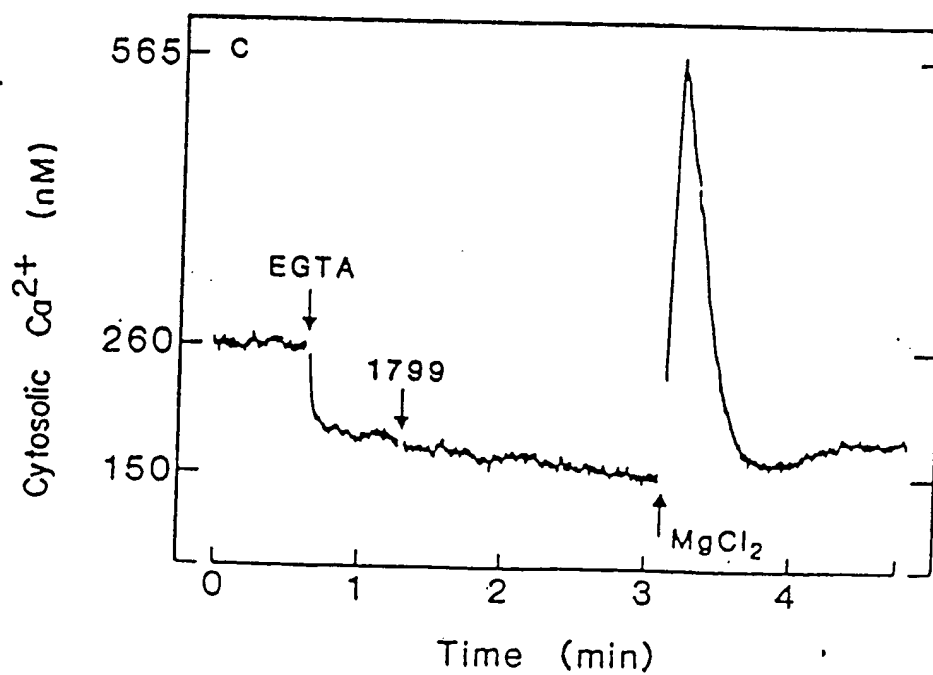


FIG. 4a.

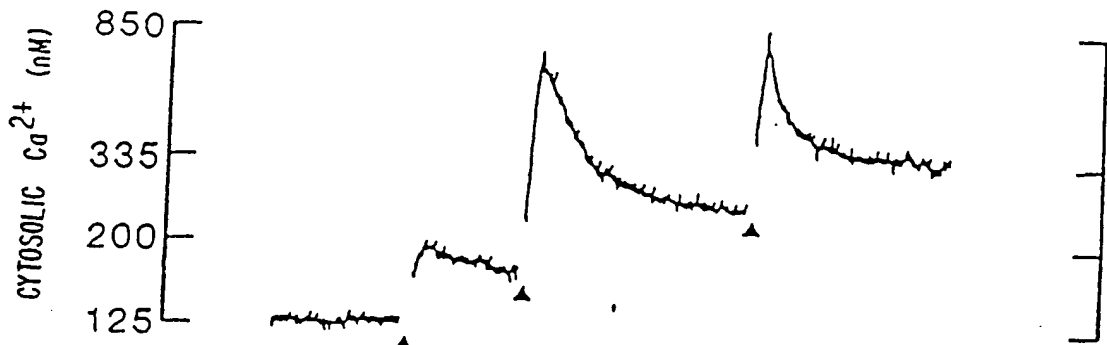


FIG. 4b.

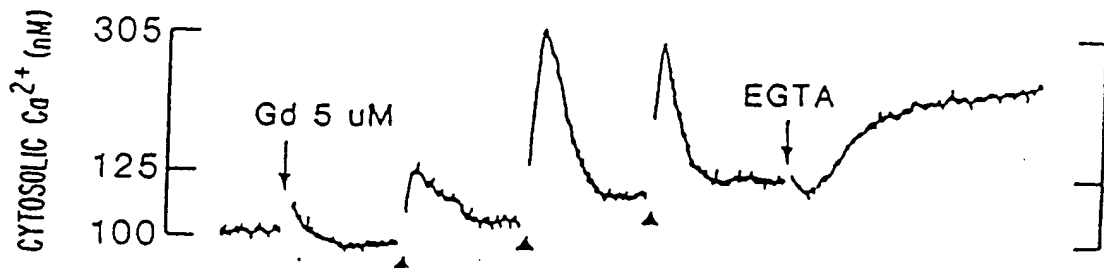


FIG. 4c.

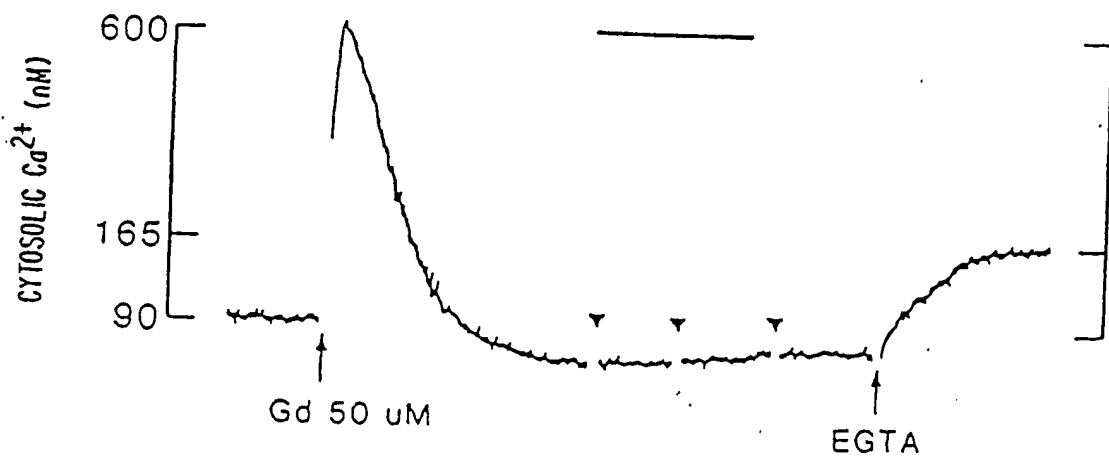


FIG. 5a.

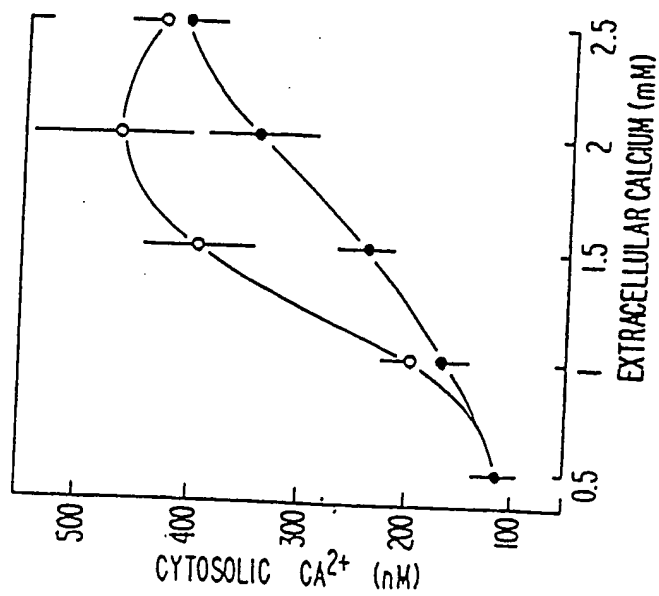


FIG. 5b.

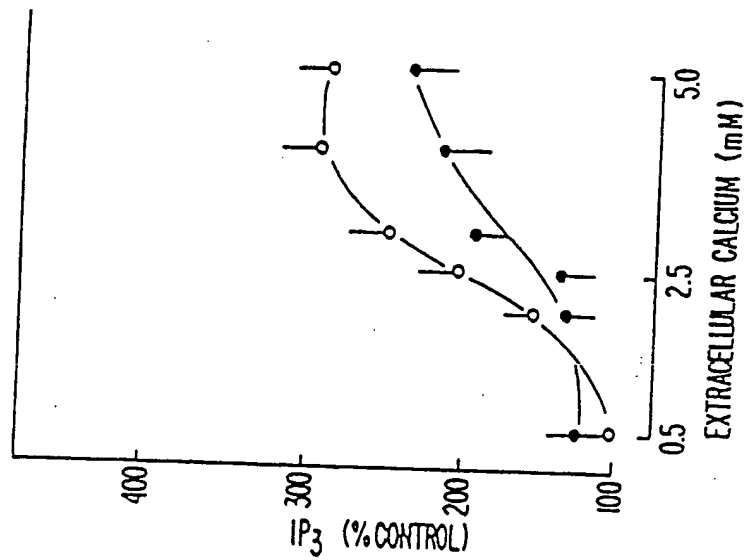
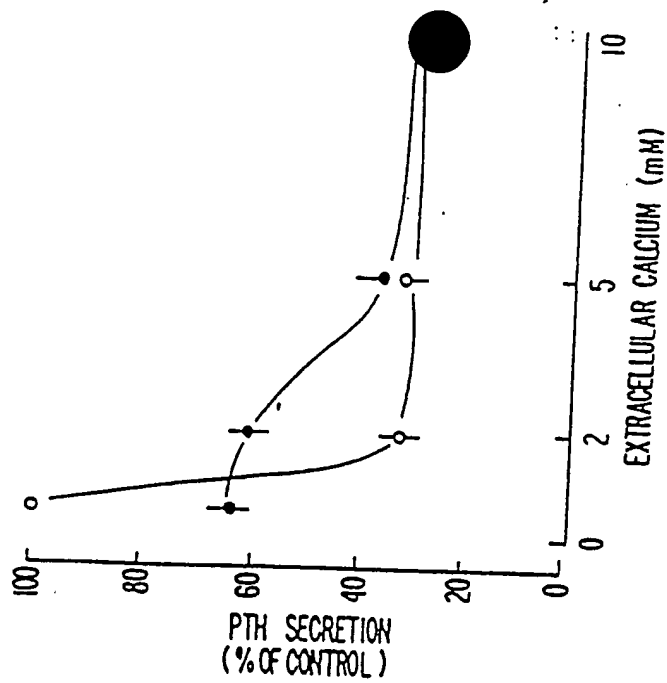


FIG. 5c.



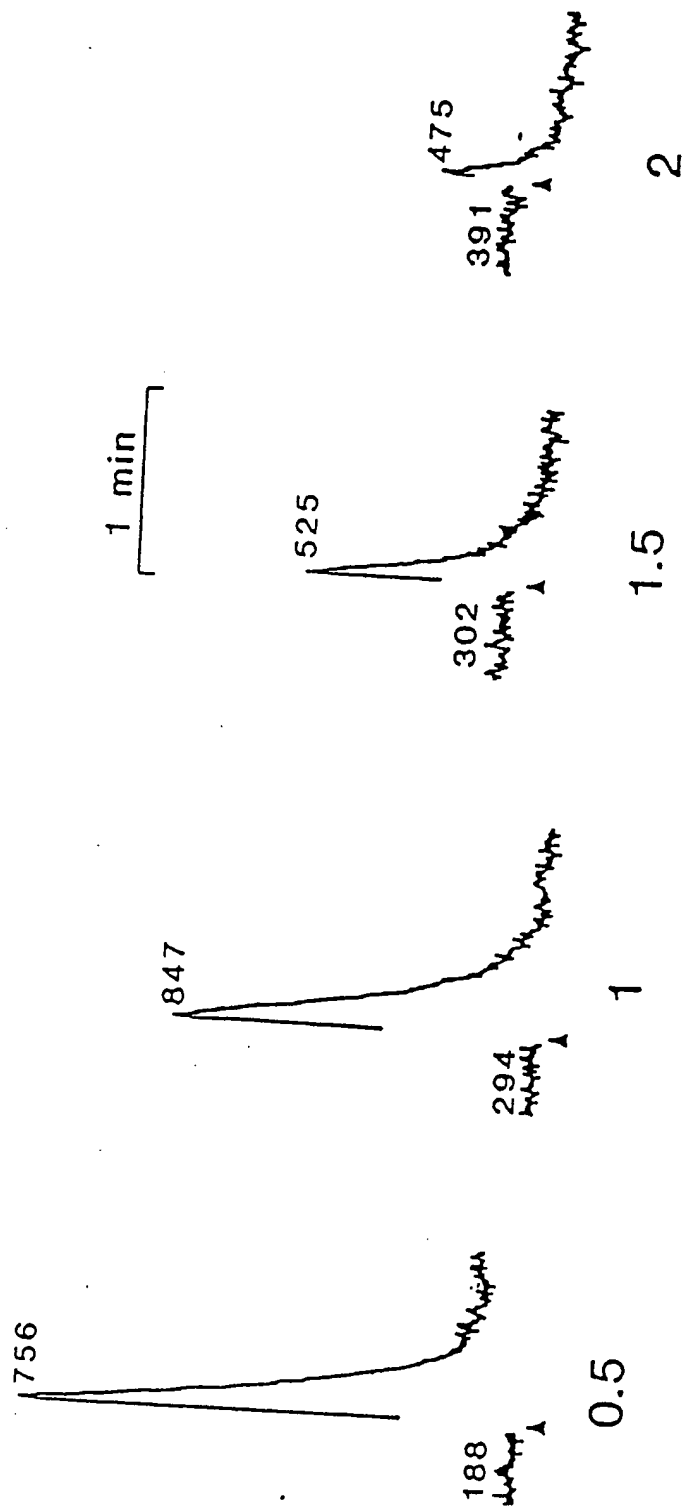


FIG. 6.

Symbol	Definition	Symbol	Definition
\mathcal{A}	Algebra	\mathcal{B}	Algebra
\mathcal{C}	Category	\mathcal{D}	Category
\mathcal{E}	Category	\mathcal{F}	Category
\mathcal{G}	Category	\mathcal{H}	Category
\mathcal{I}	Category	\mathcal{J}	Category
\mathcal{K}	Category	\mathcal{L}	Category
\mathcal{M}	Category	\mathcal{N}	Category
\mathcal{O}	Category	\mathcal{P}	Category
\mathcal{Q}	Category	\mathcal{R}	Category
\mathcal{S}	Category	\mathcal{T}	Category
\mathcal{U}	Category	\mathcal{V}	Category
\mathcal{W}	Category	\mathcal{X}	Category
\mathcal{Y}	Category	\mathcal{Z}	Category
\mathcal{A}^*	Adjoint	\mathcal{B}^*	Adjoint
\mathcal{C}^*	Adjoint	\mathcal{D}^*	Adjoint
\mathcal{E}^*	Adjoint	\mathcal{F}^*	Adjoint
\mathcal{G}^*	Adjoint	\mathcal{H}^*	Adjoint
\mathcal{I}^*	Adjoint	\mathcal{J}^*	Adjoint
\mathcal{K}^*	Adjoint	\mathcal{L}^*	Adjoint
\mathcal{M}^*	Adjoint	\mathcal{N}^*	Adjoint
\mathcal{O}^*	Adjoint	\mathcal{P}^*	Adjoint
\mathcal{Q}^*	Adjoint	\mathcal{R}^*	Adjoint
\mathcal{S}^*	Adjoint	\mathcal{T}^*	Adjoint
\mathcal{U}^*	Adjoint	\mathcal{V}^*	Adjoint
\mathcal{W}^*	Adjoint	\mathcal{X}^*	Adjoint
\mathcal{Y}^*	Adjoint	\mathcal{Z}^*	Adjoint

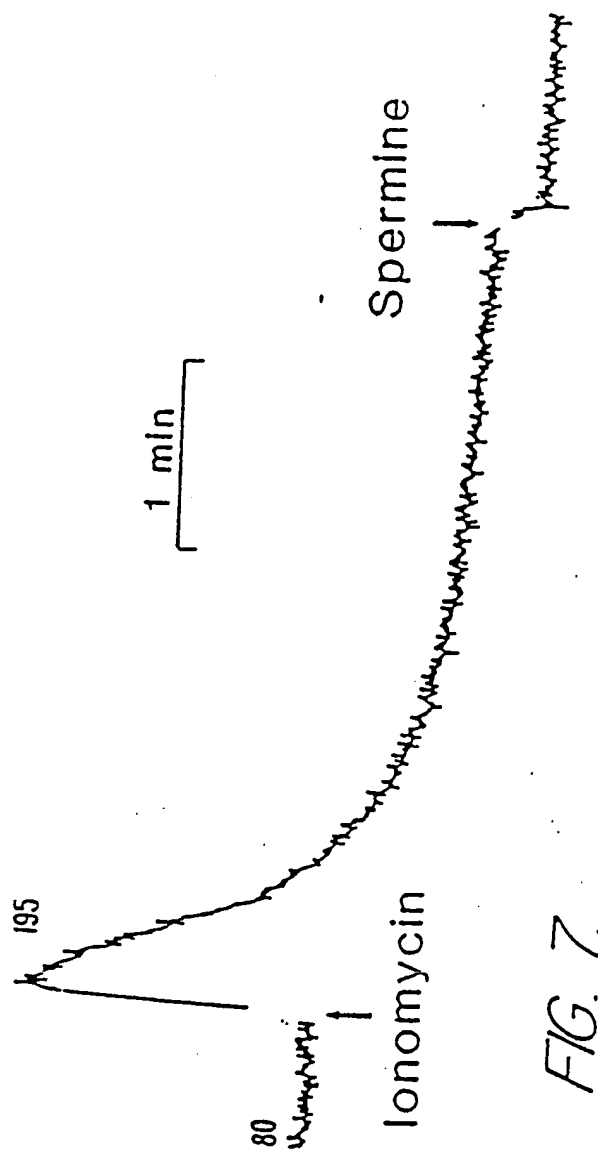
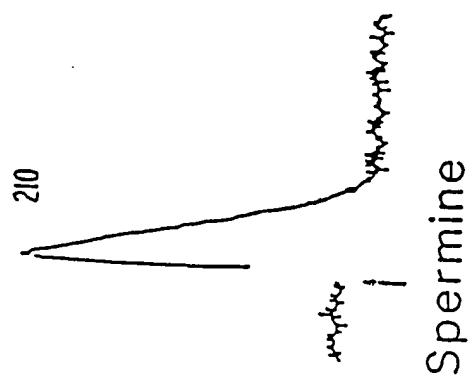


FIG. 7.

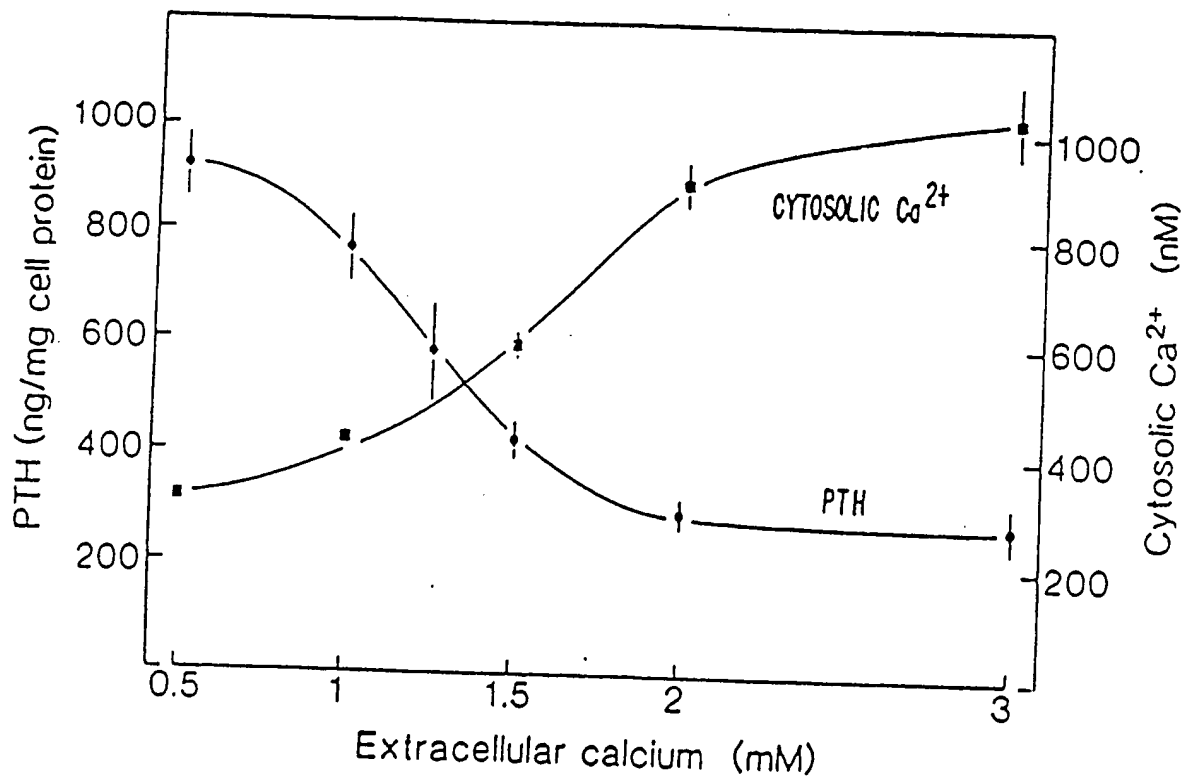
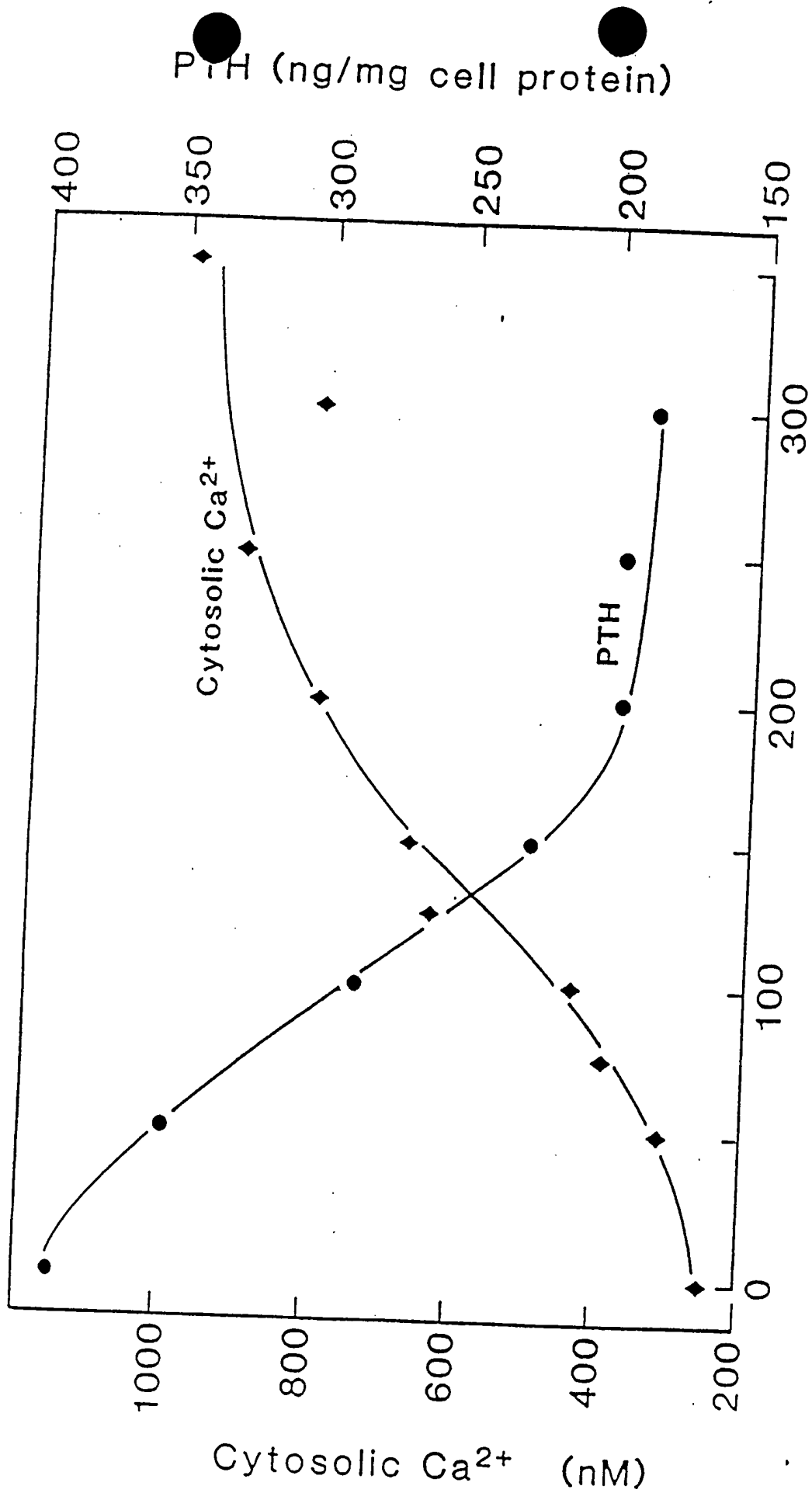


FIG. 8a.

[illegible]

Spermine (μM)

FIG. 9a.

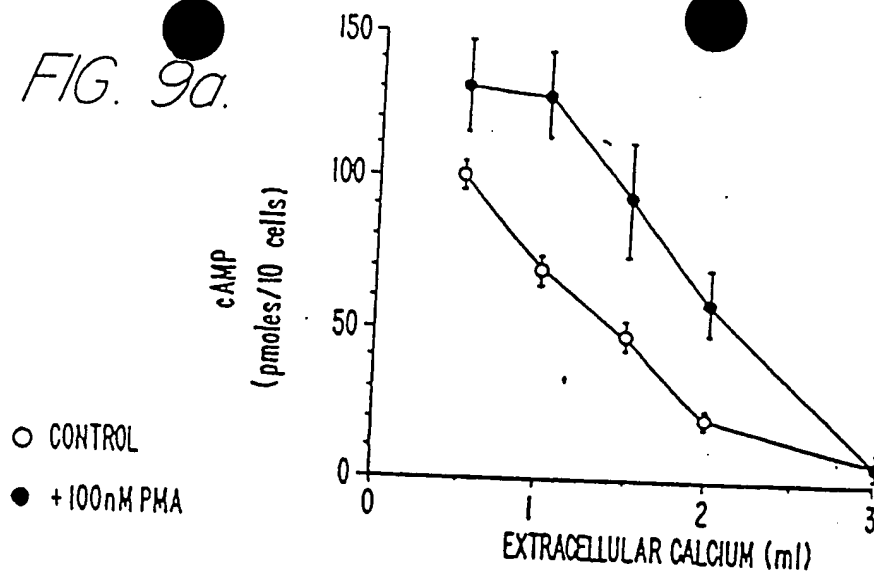


FIG. 9b.

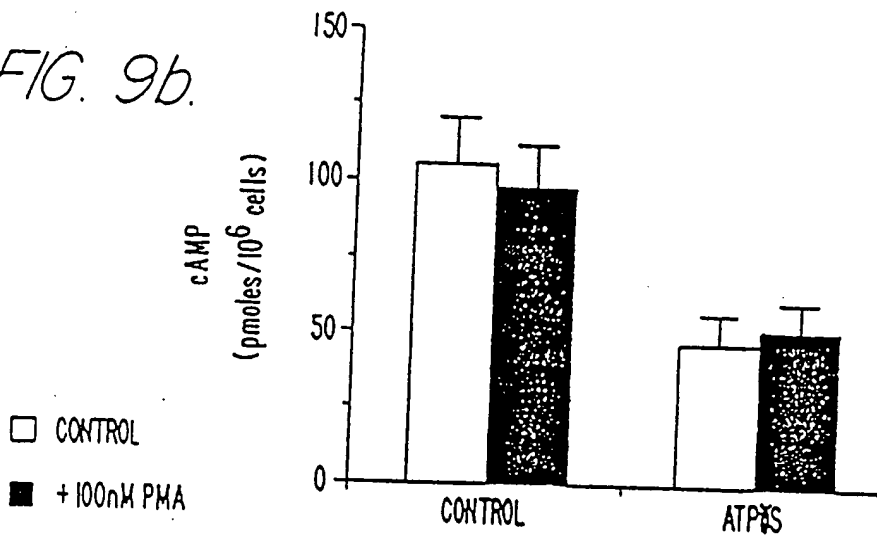


FIG. 9c.

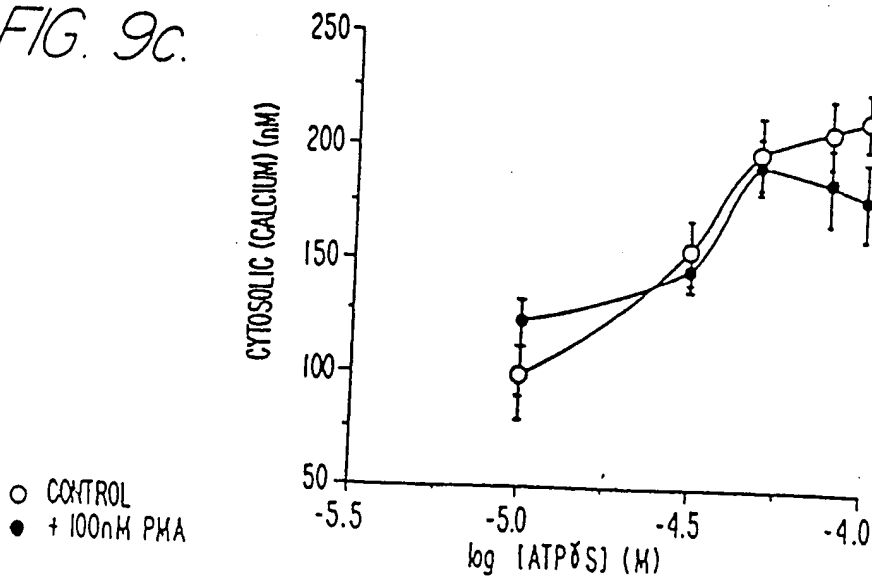


FIG. 10a.

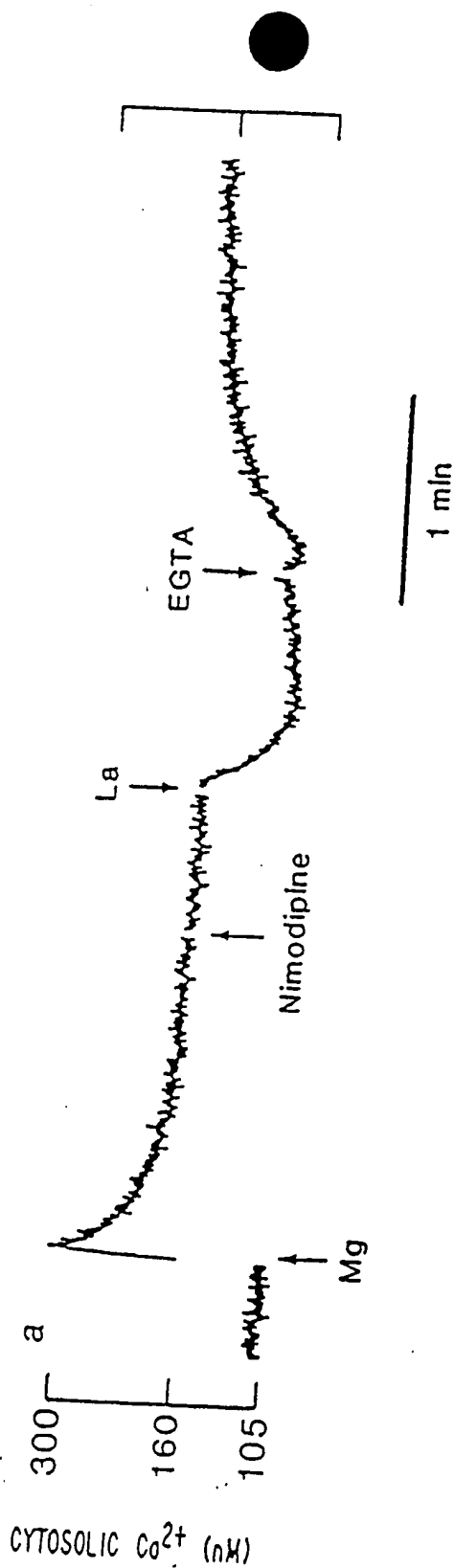
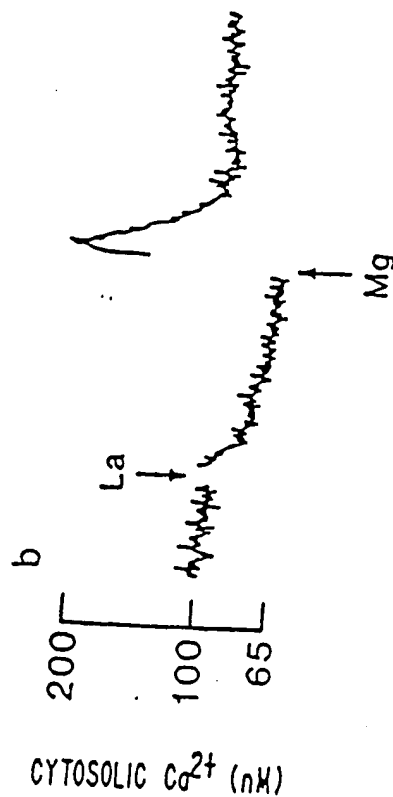


FIG. 10b.



c

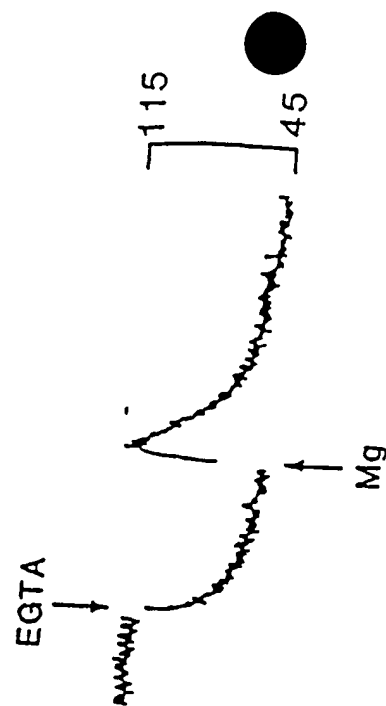


FIG. 10c.

FIG. 11a.

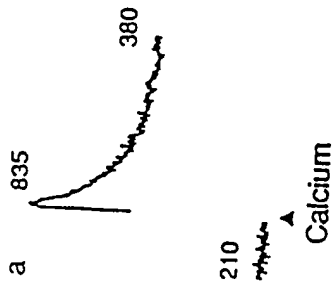


FIG. 11b.



FIG. 11c.



FIG. 11d.



FIG. 11e.

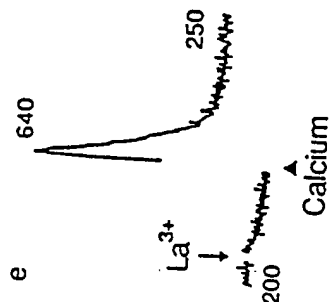


FIG. 11f.

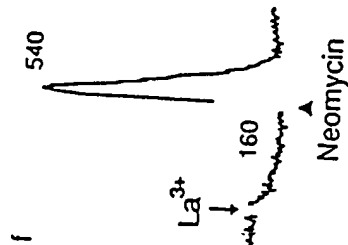


FIG. 11g.

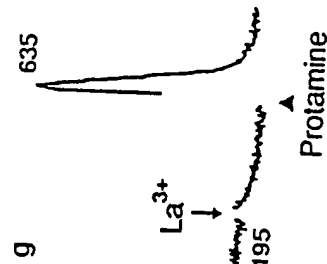


FIG. 11h.

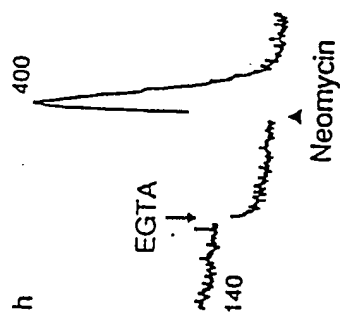


FIG. 11i.

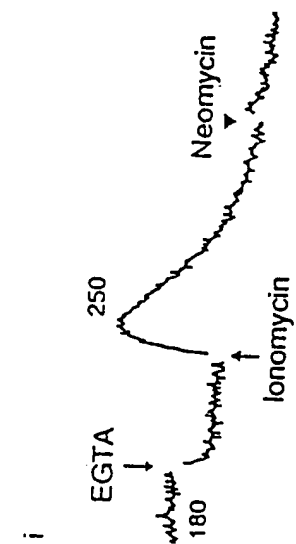


FIG. 12.

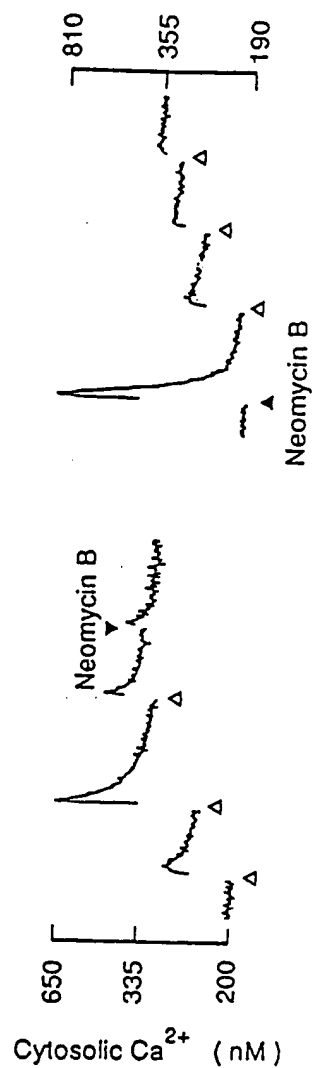


FIG. 13a.

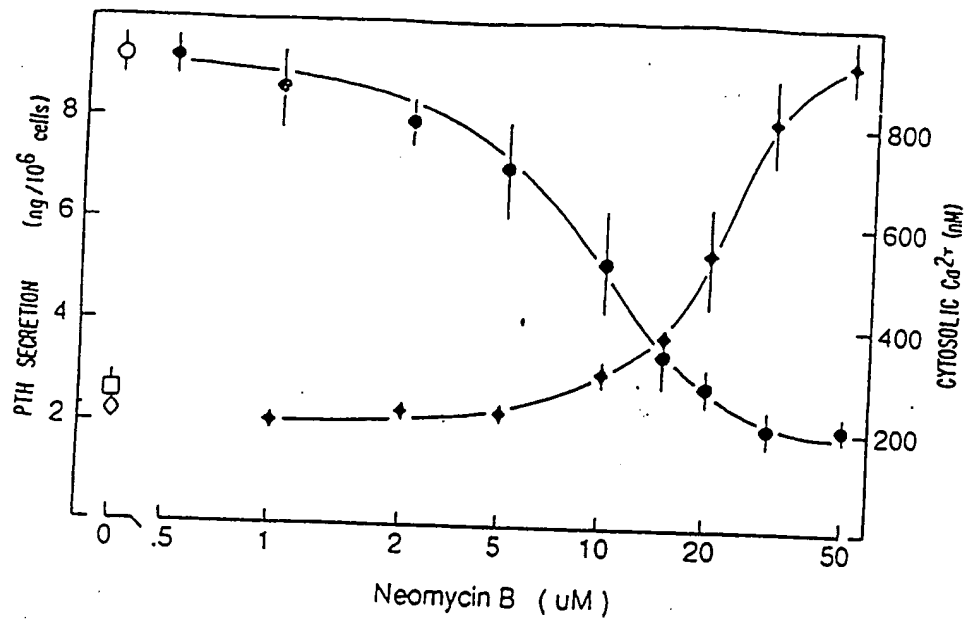


FIG. 13b.

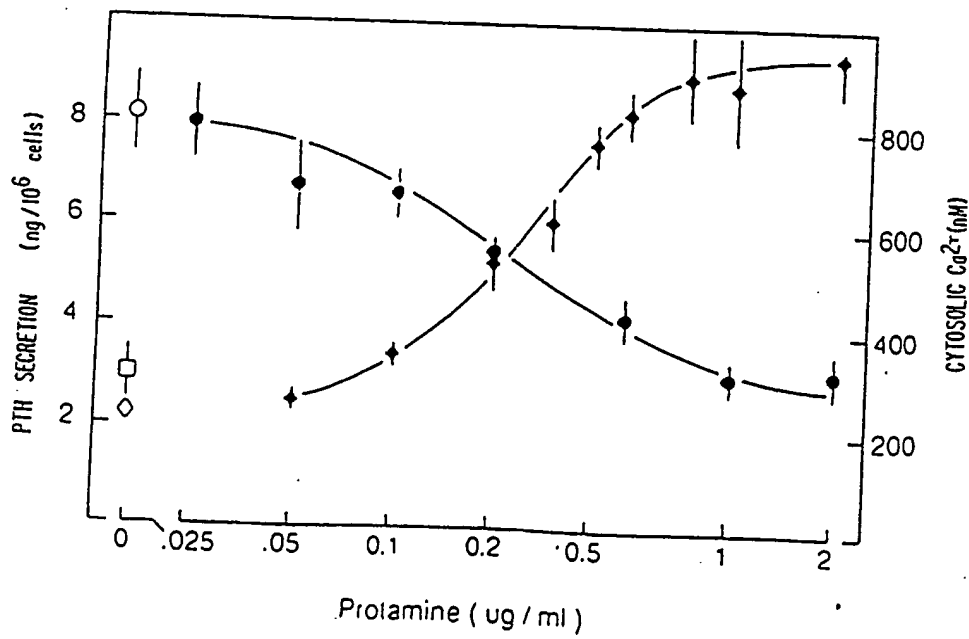


FIG. 14.

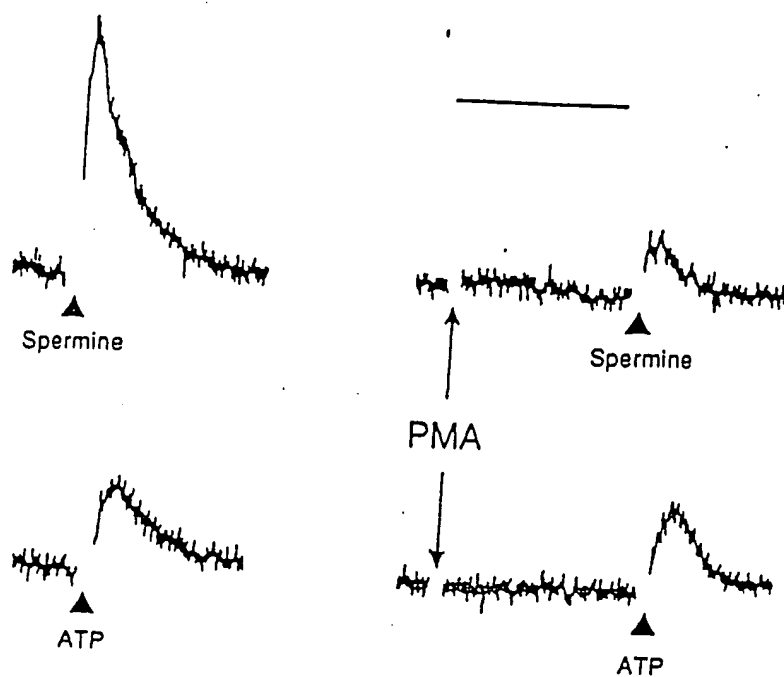


FIG. 15a.

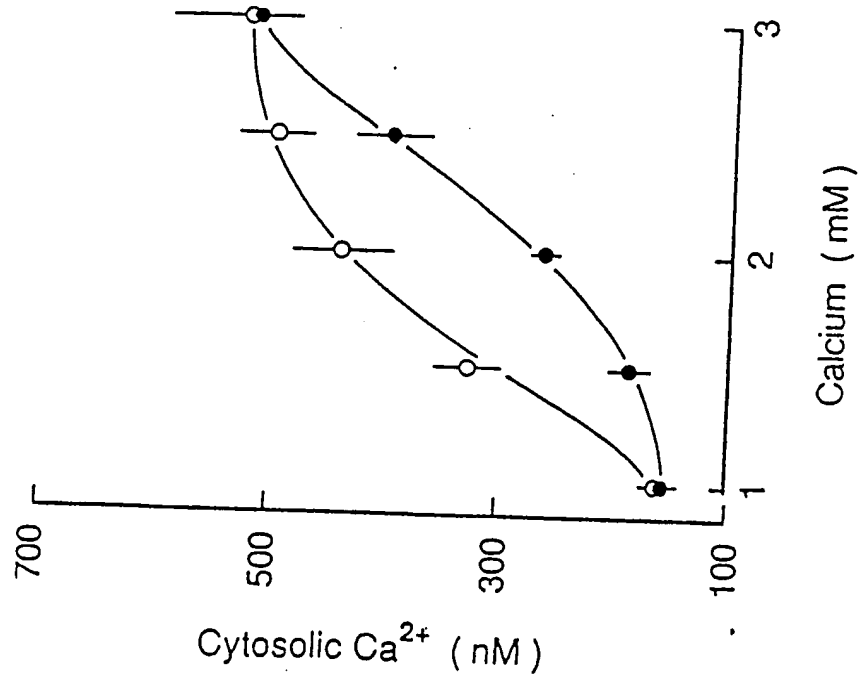
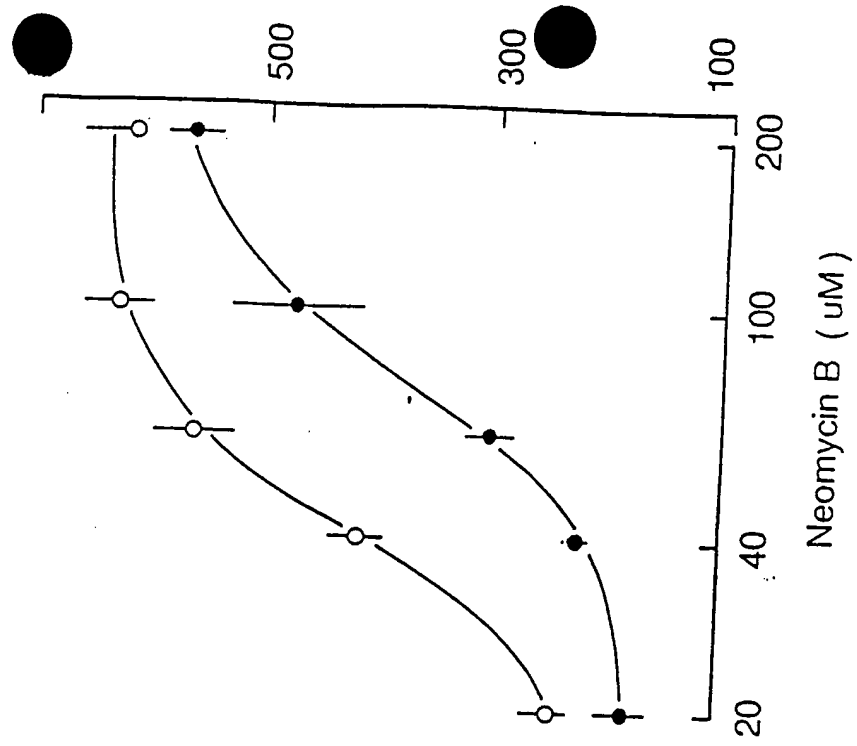


FIG. 15b.



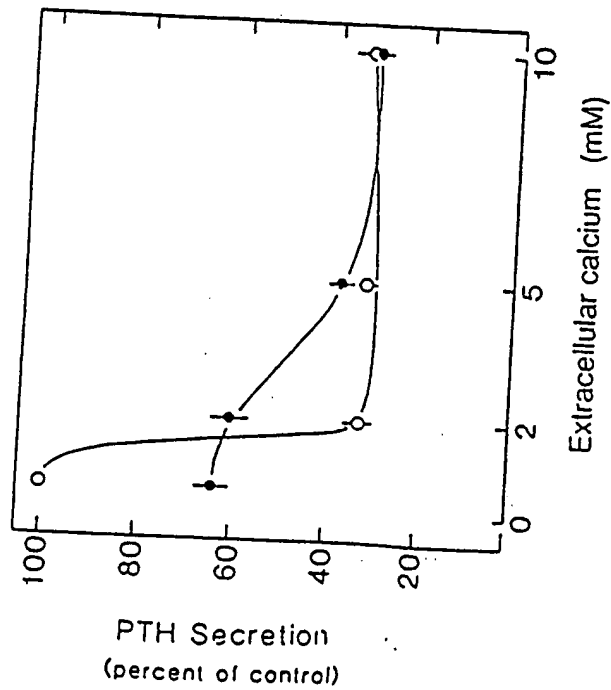


FIG. 16a.

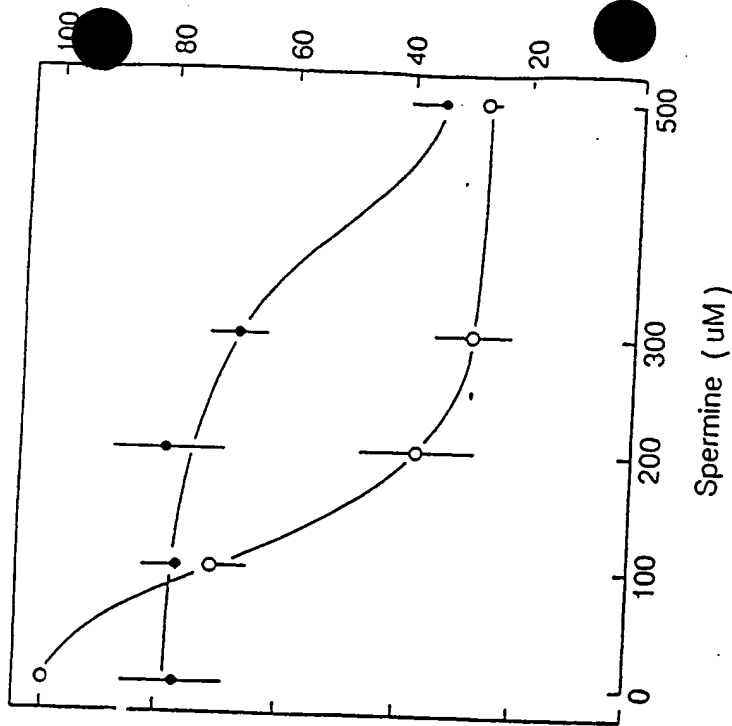


FIG. 16b.

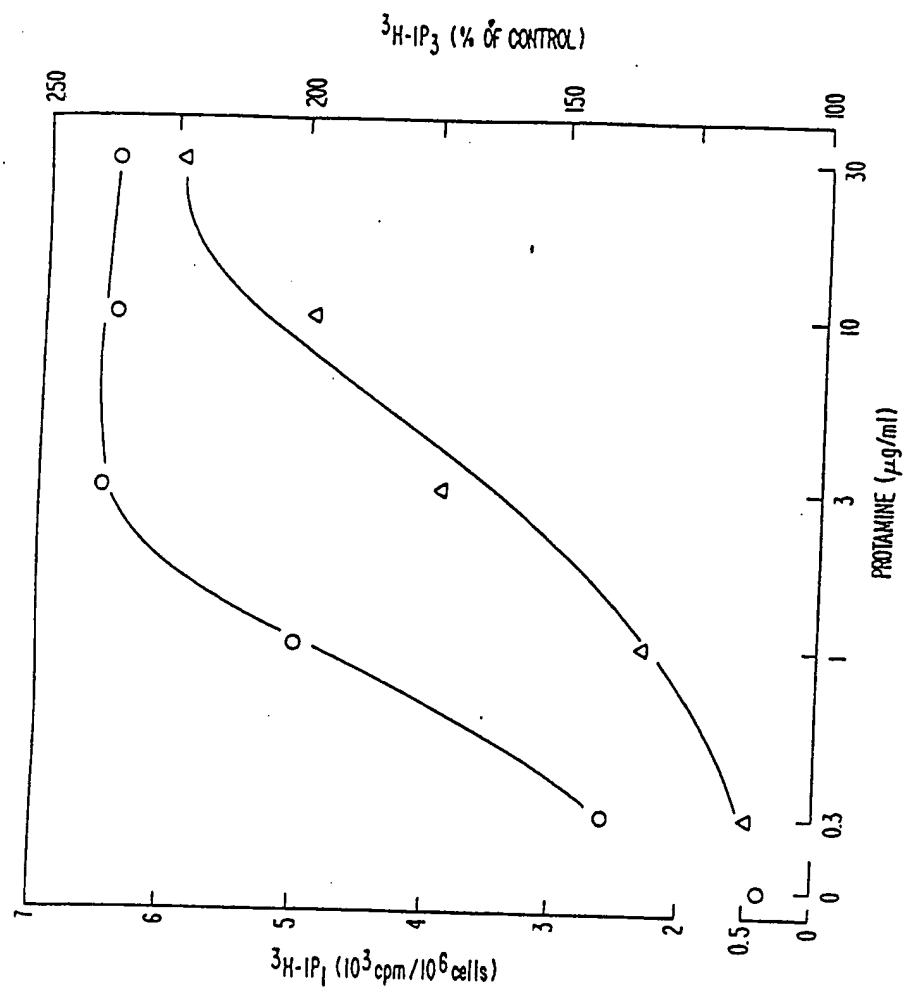


FIG. 17.

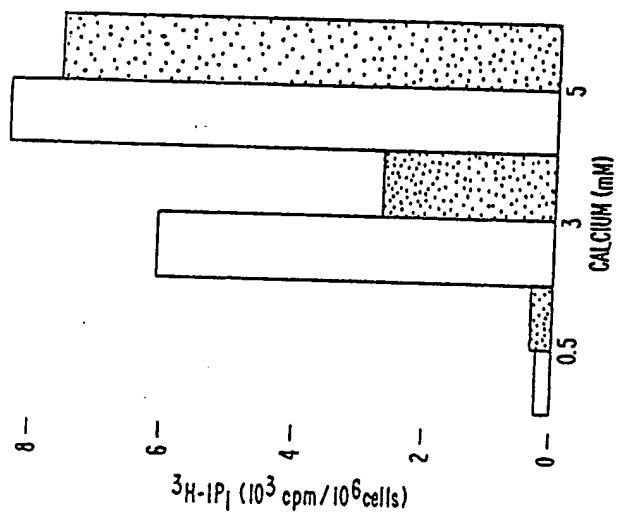


FIG. 18a.

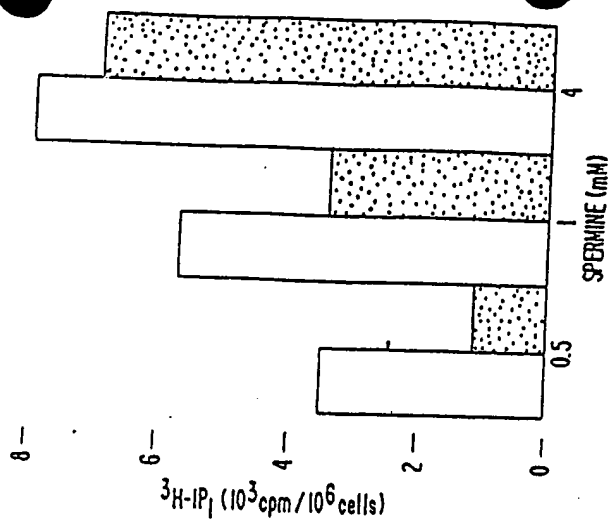


FIG. 18b.

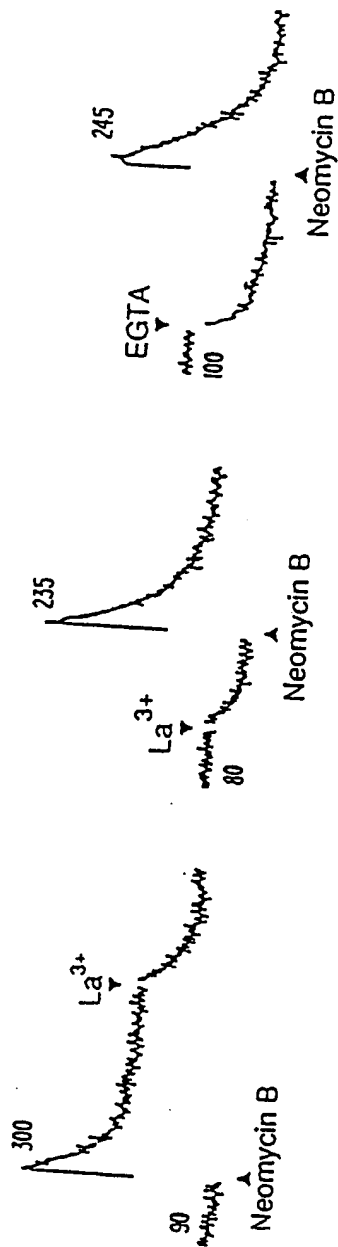


FIG. 19.

FIG. 20a.

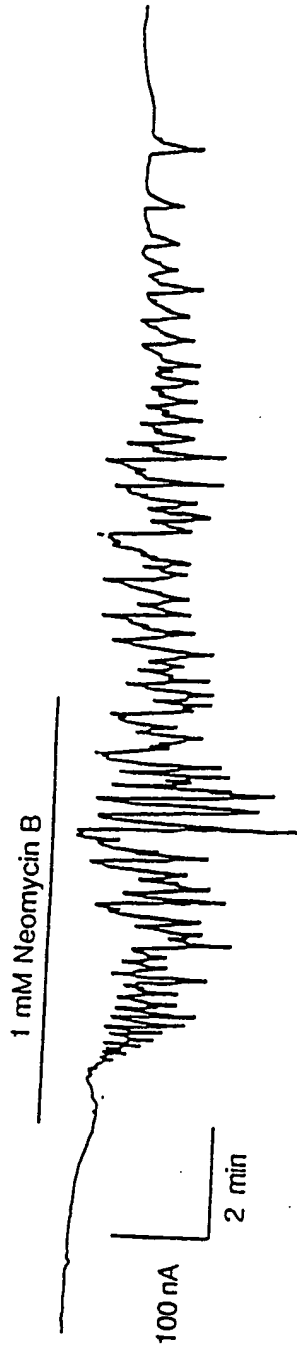


FIG. 20b.

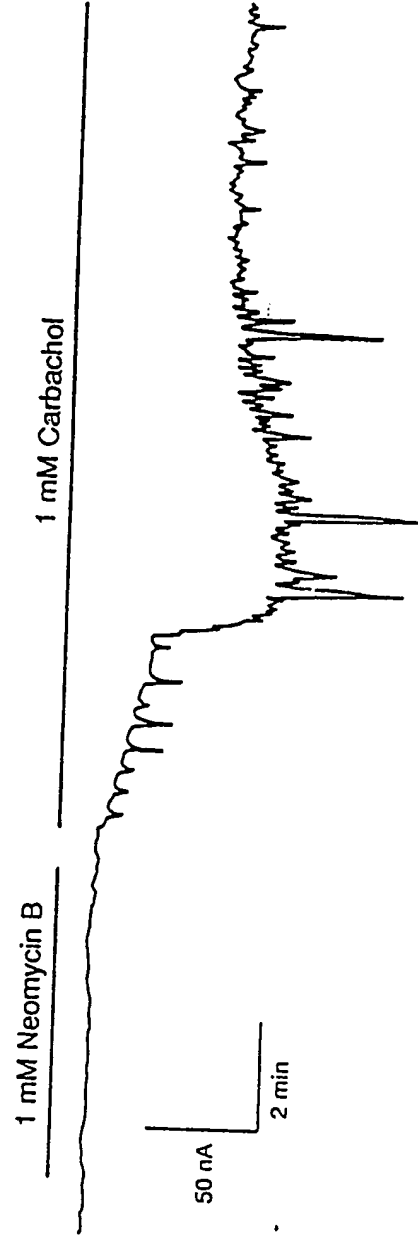


FIG. 21.

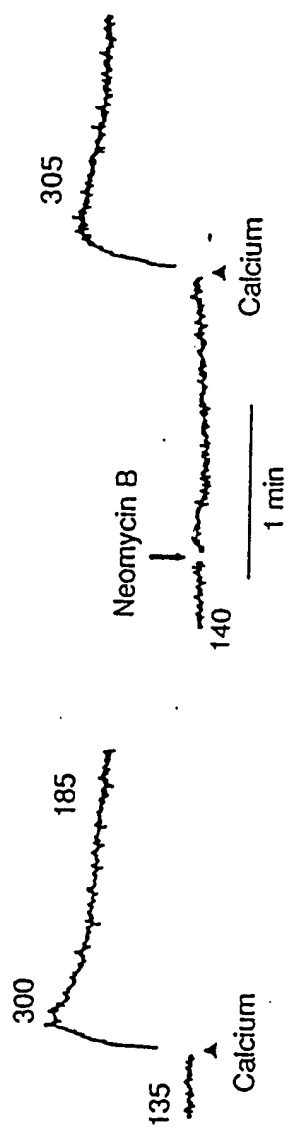


FIG. 22.

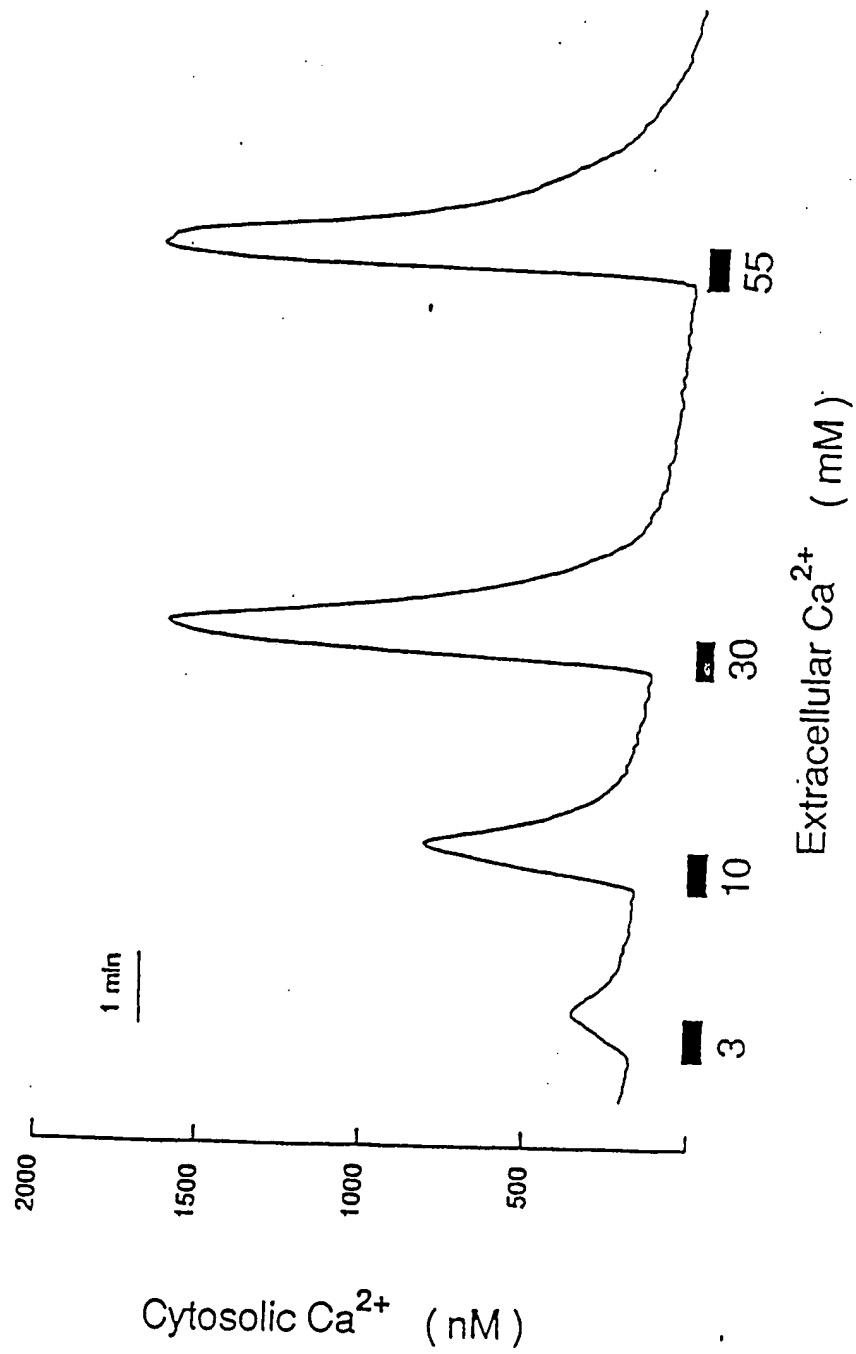


FIG. 23.

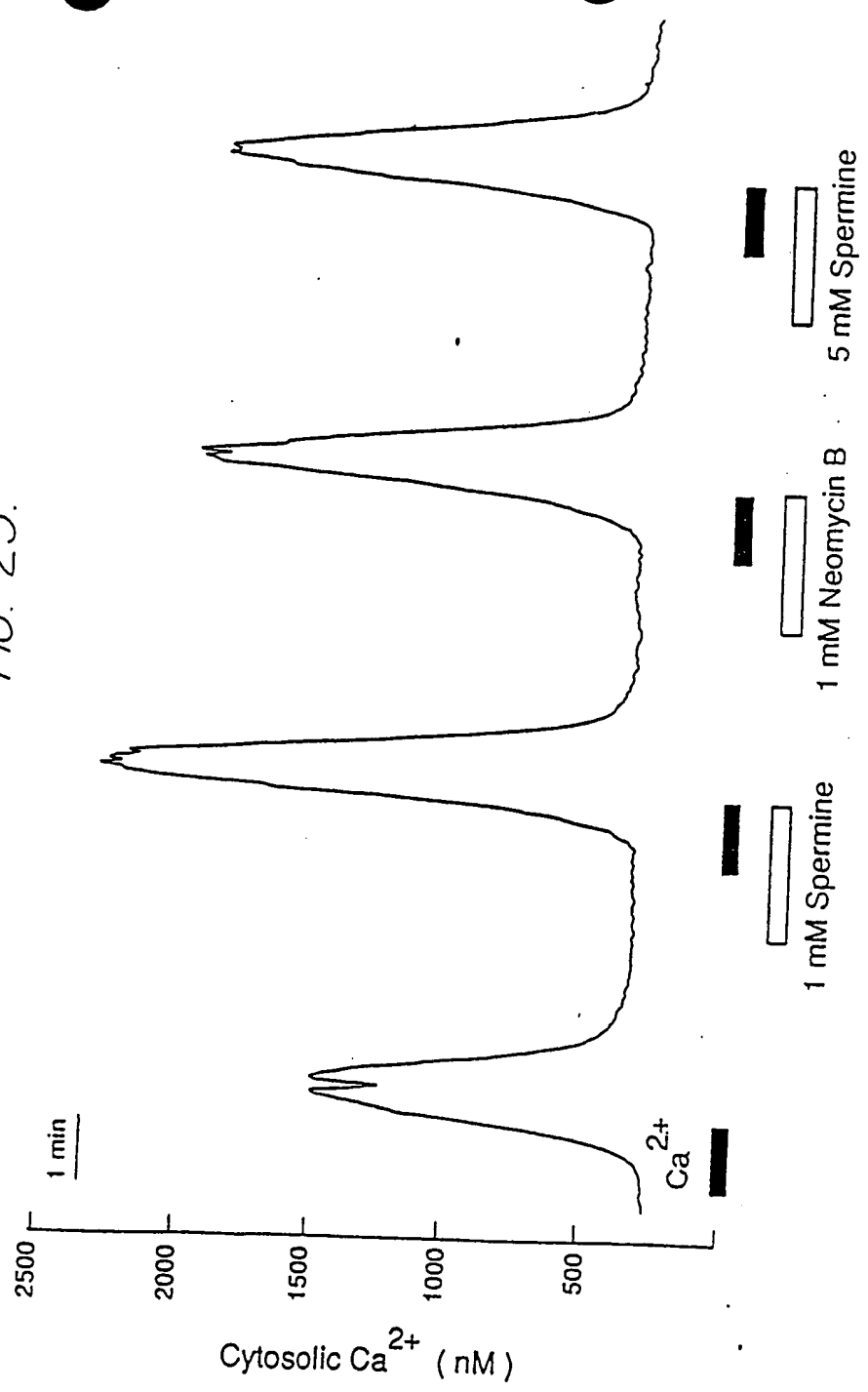


FIG. 24.

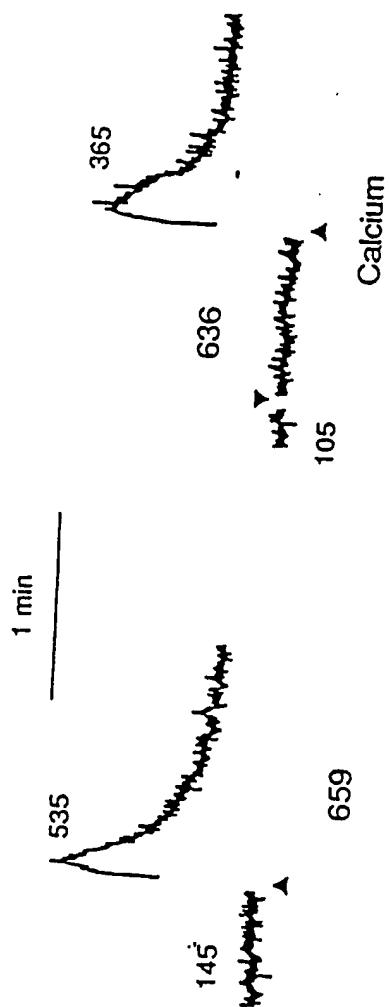


FIG. 25a.

10 mM Mg^{2+}



FIG. 25b.

600 μM Gd^{3+}

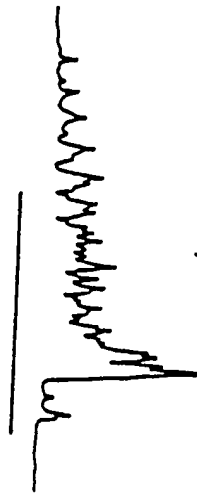


FIG. 25c.

10 mM Mg^{2+}

100 nM Substance K



FIG. 26.

10 mM Calcium

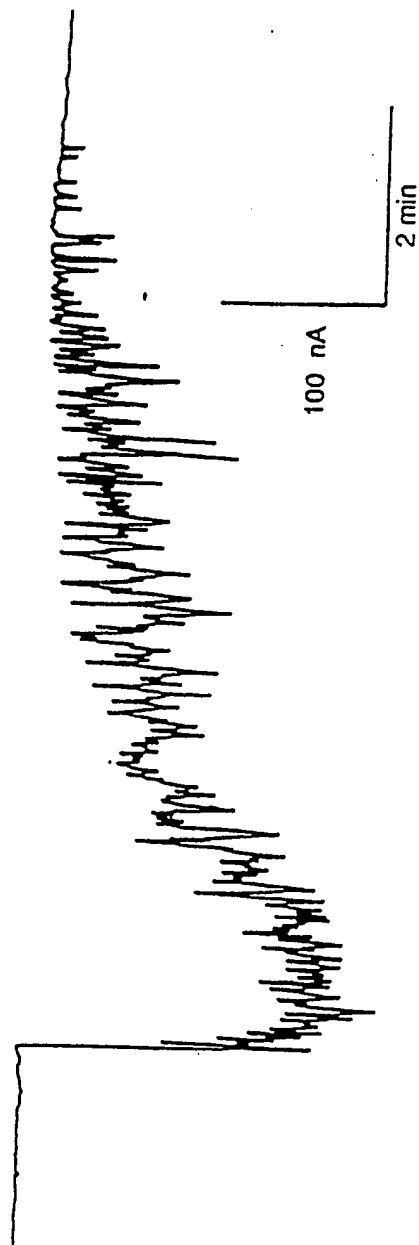
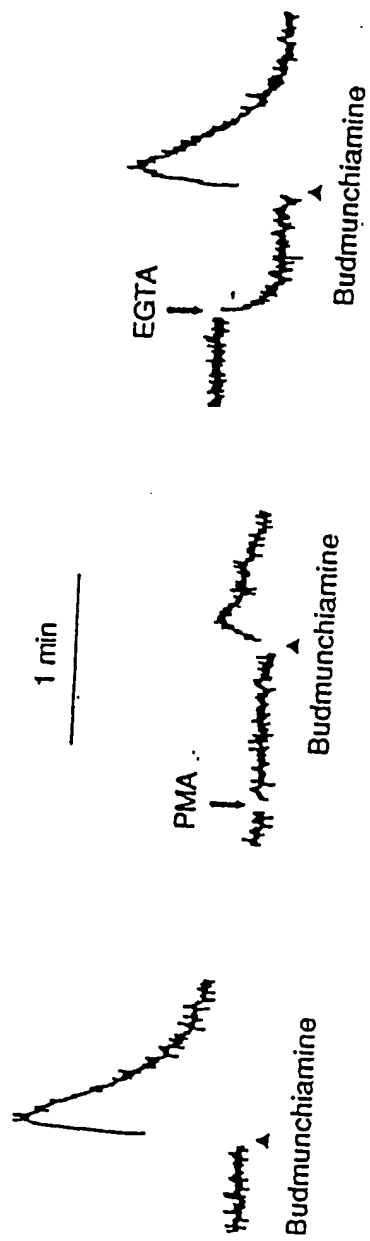
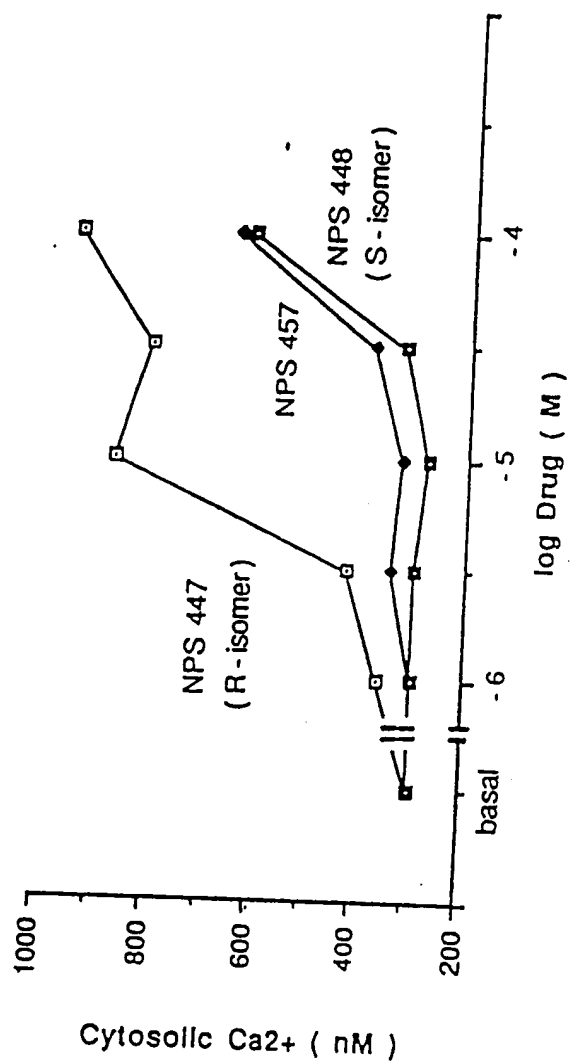


FIG. 27.



cytosolic Ca^{2+} (nM)

FIG. 28a.



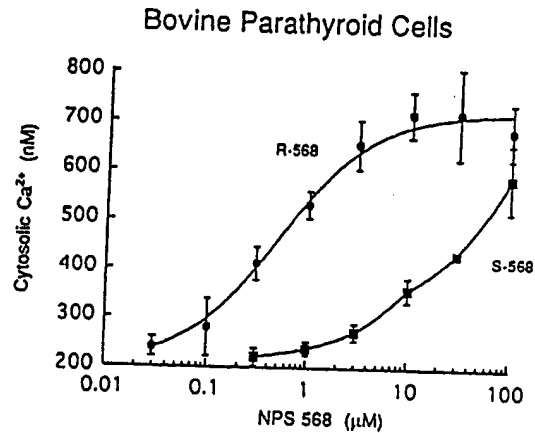
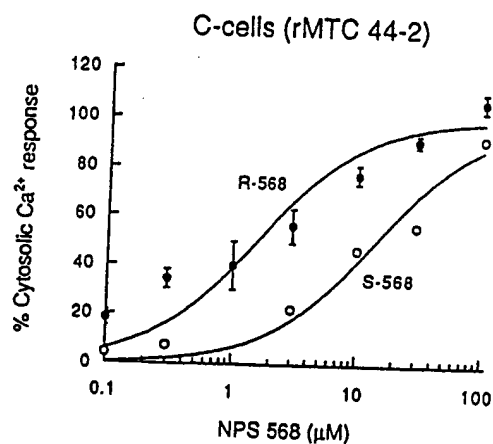
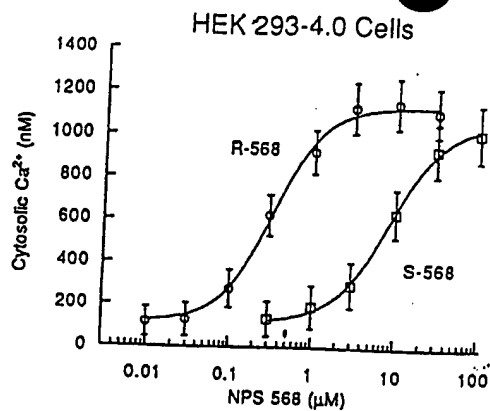


FIG. 28b.

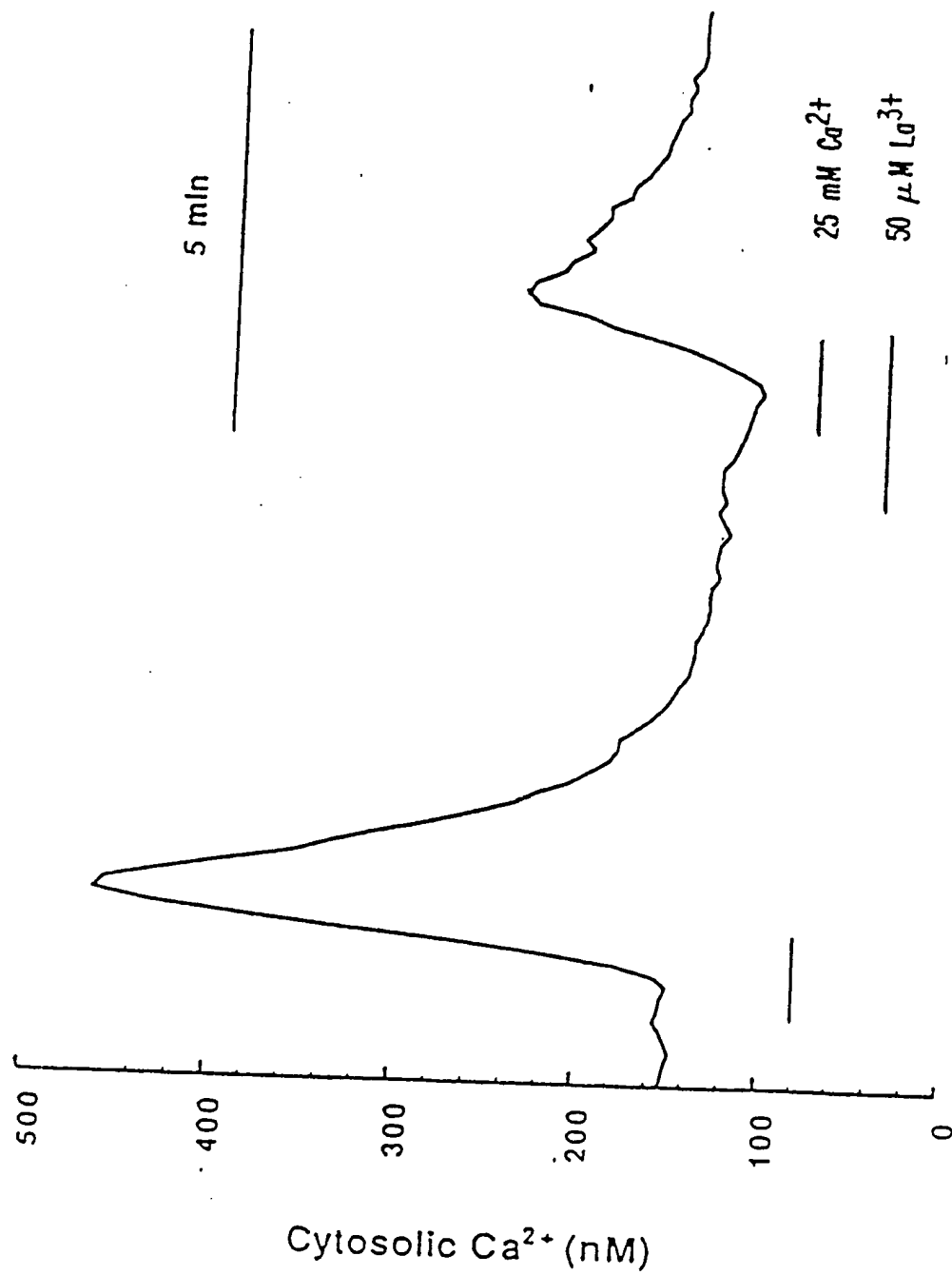
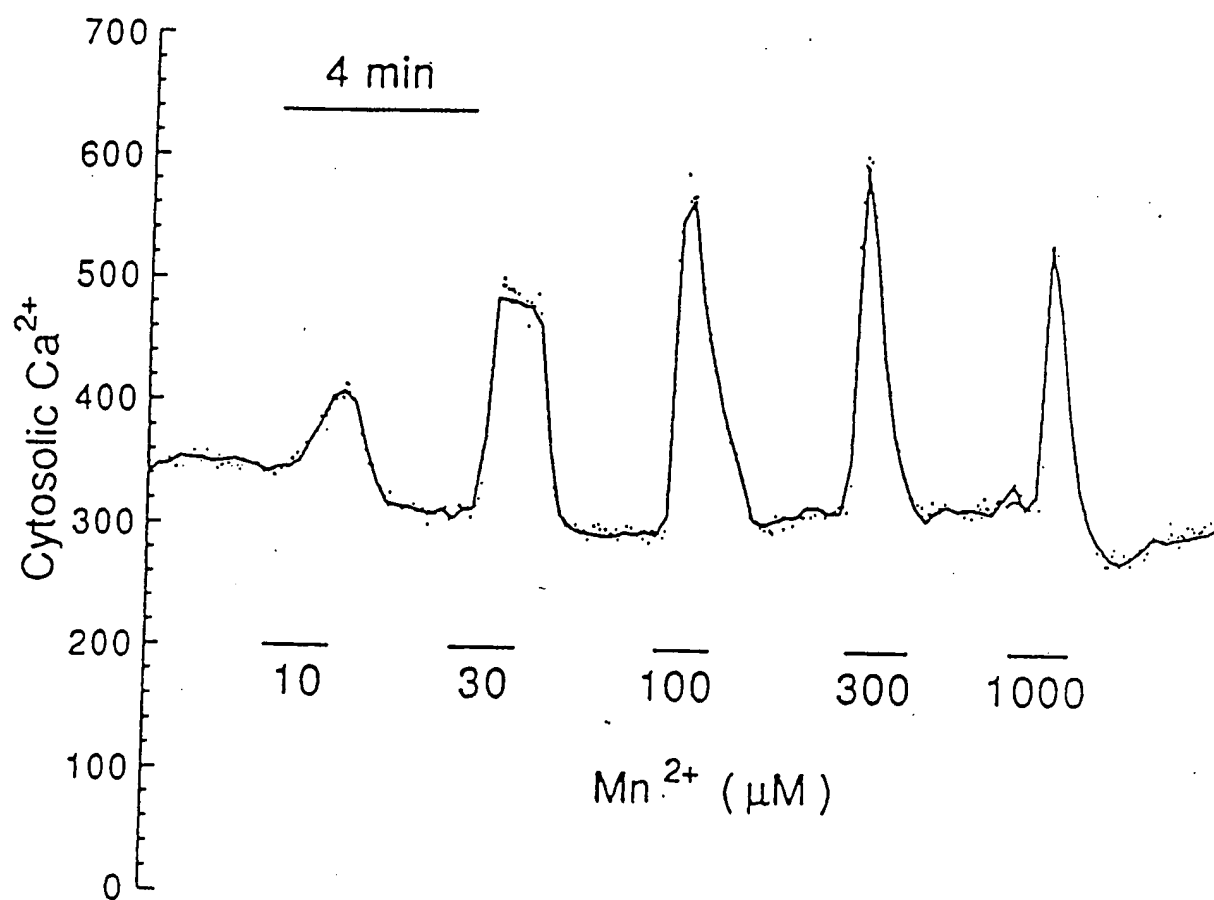


FIG. 29.

FIG. 30a.



(a.)

1. The first part of the document is a list of references. The references are listed in a vertical column, with the first reference at the top and the last reference at the bottom. The references are:

- 1. The first part of the document is a list of references. The references are listed in a vertical column, with the first reference at the top and the last reference at the bottom. The references are:

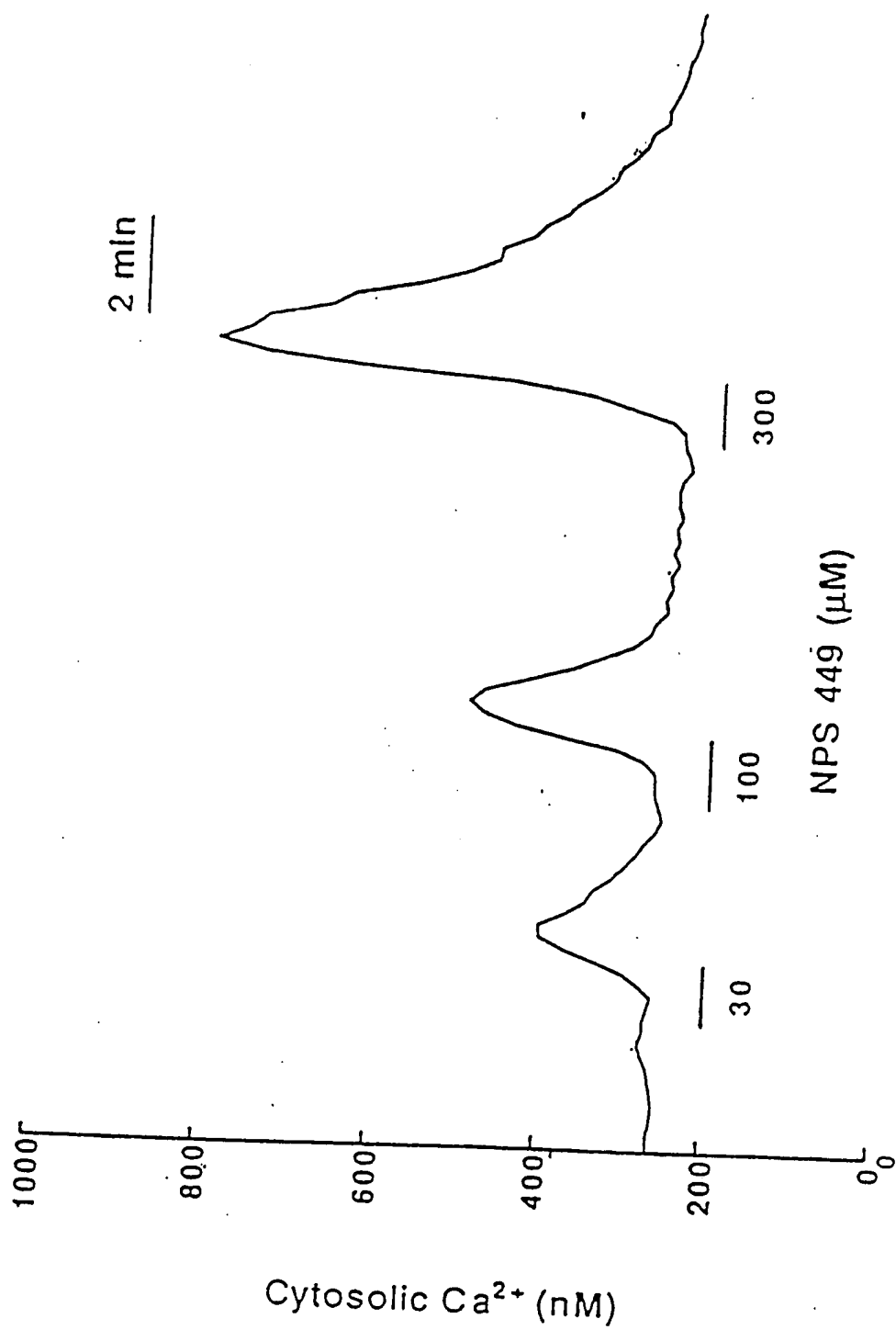


FIG. 31a.

Ca²⁺ release

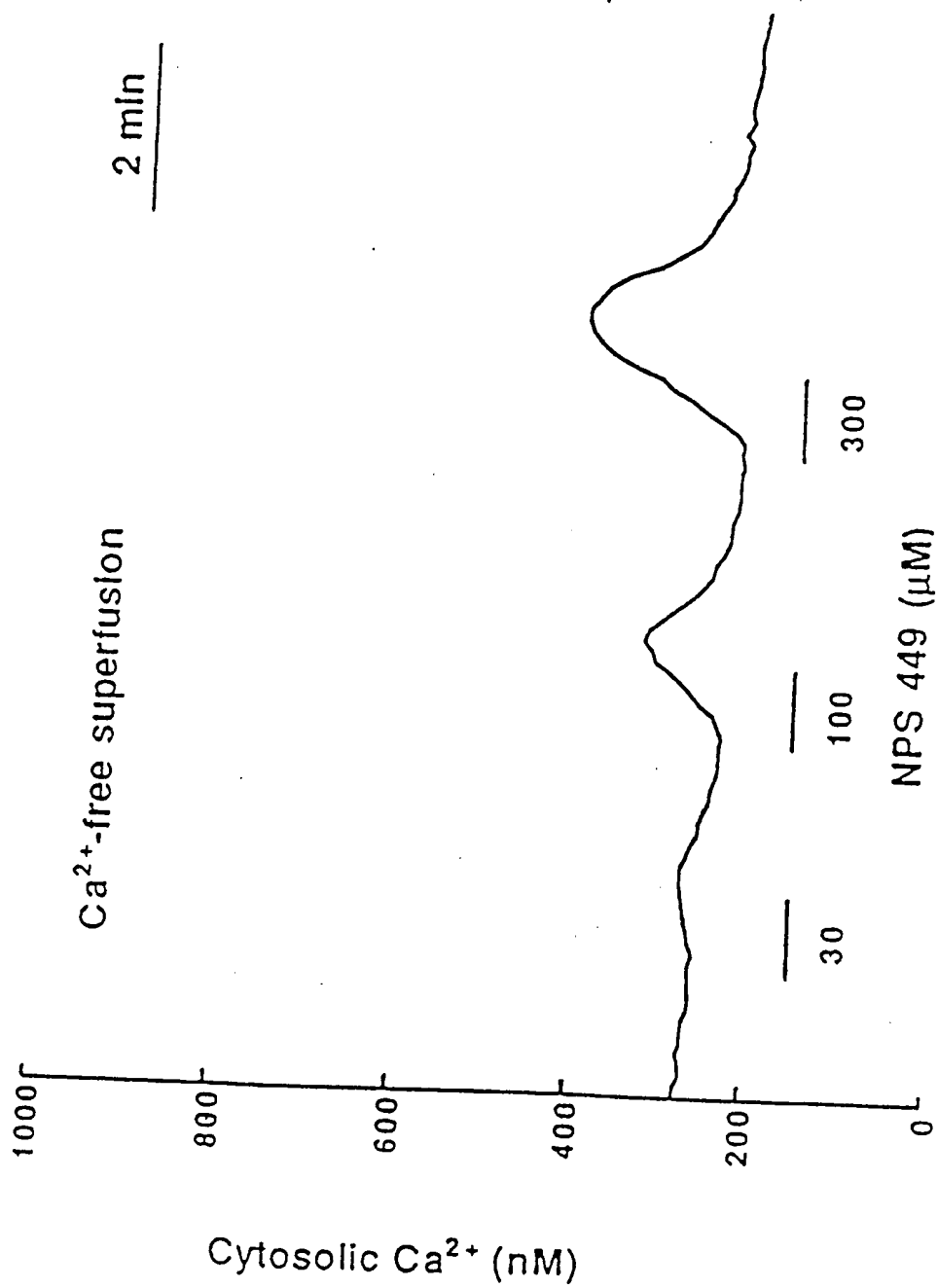


FIG. 31b.

140

45

NPS 019

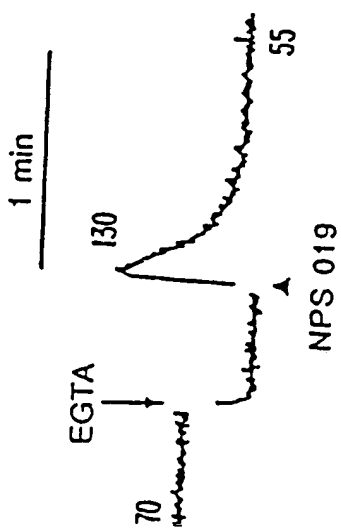
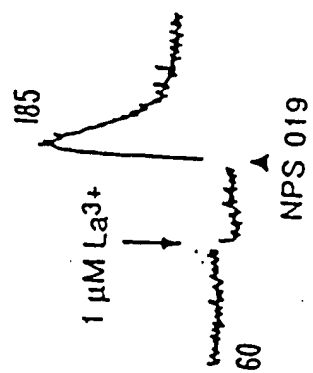


FIG. 32.

FIG. 33.

100 μ M NPS 456

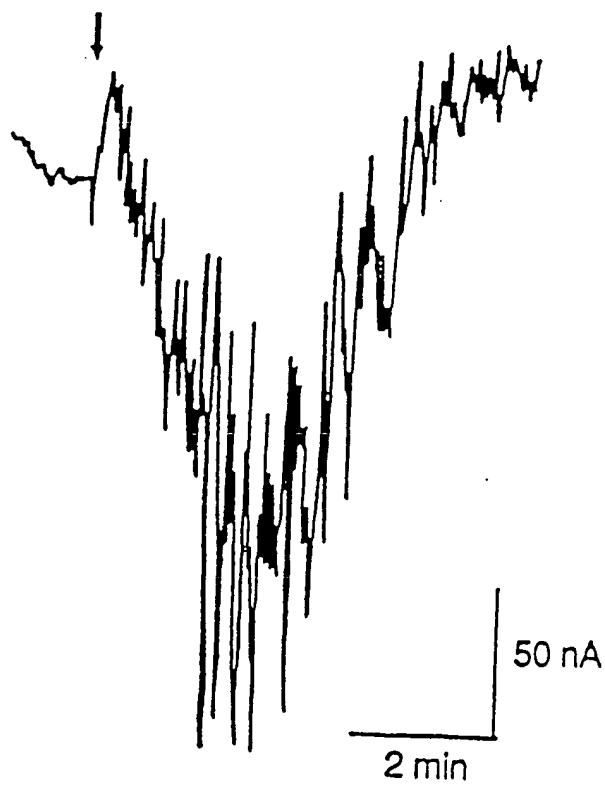
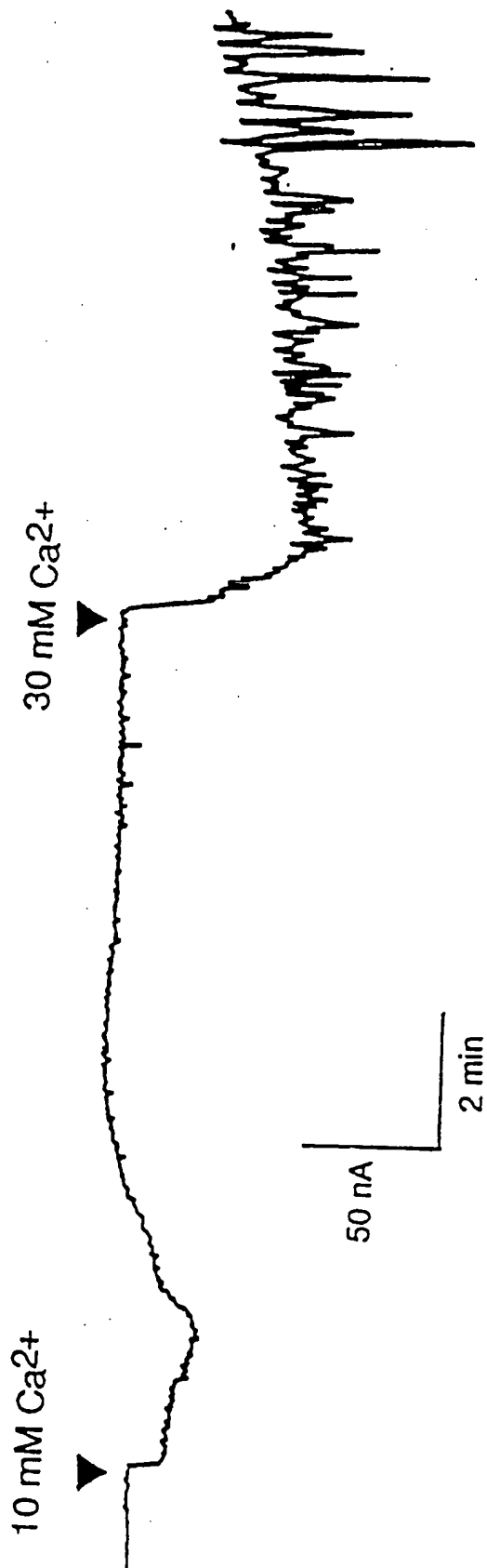


FIG. 34.



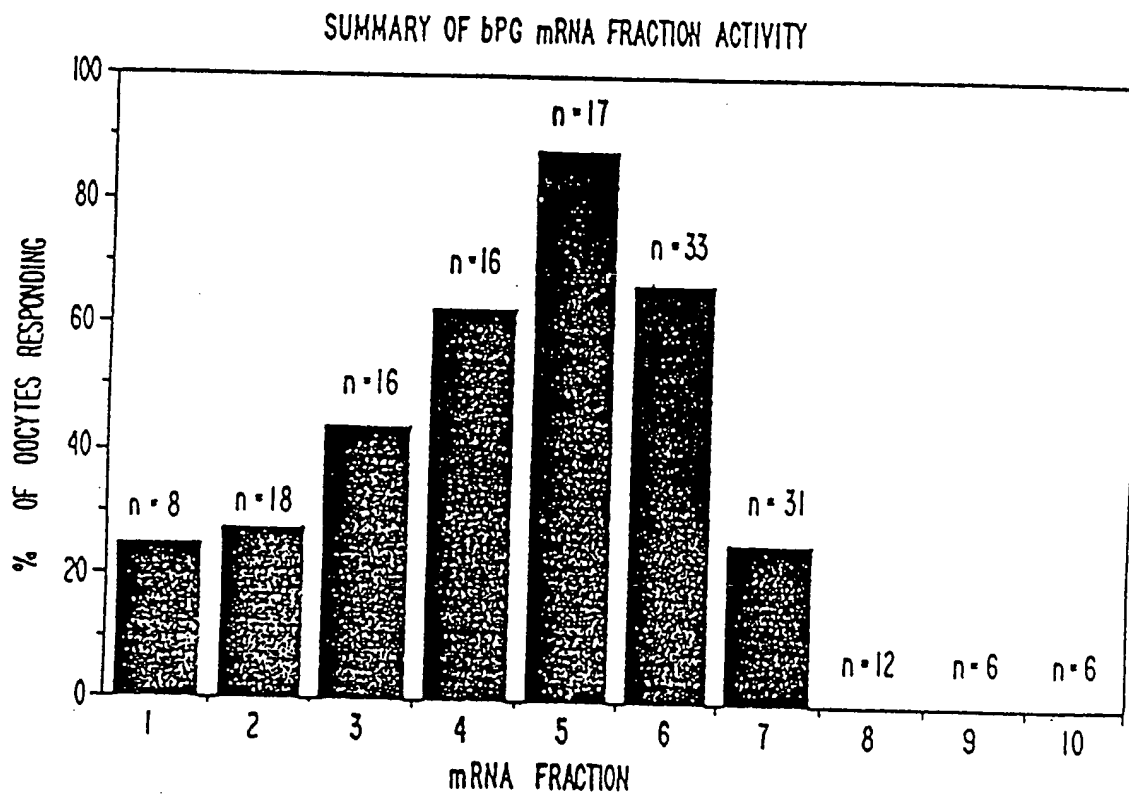


FIG. 35.

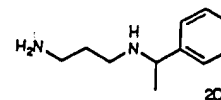
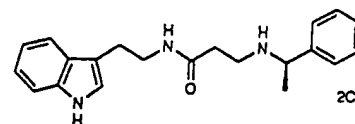
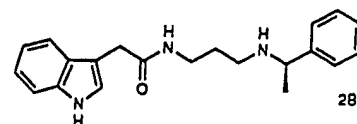
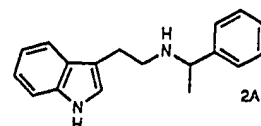
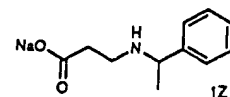
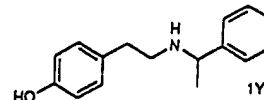
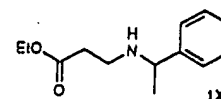
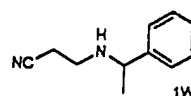
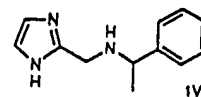
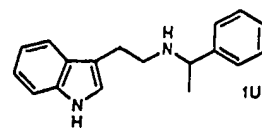
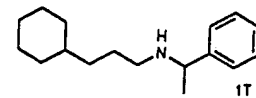
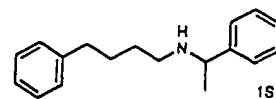
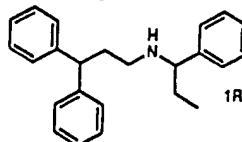
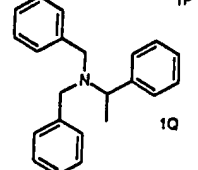
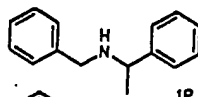
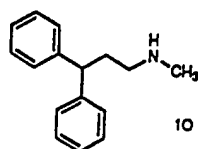
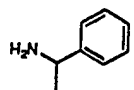
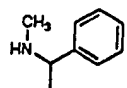
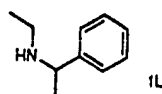
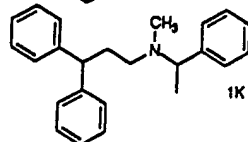
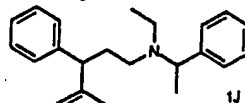
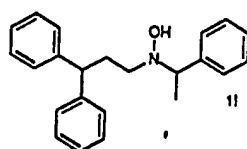
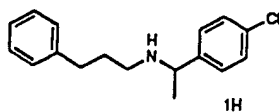
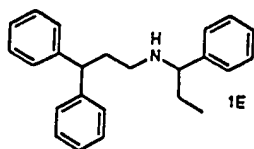
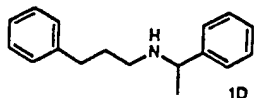
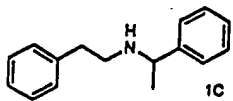
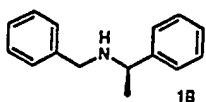
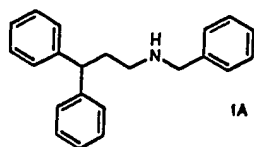
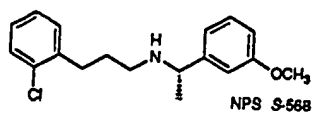
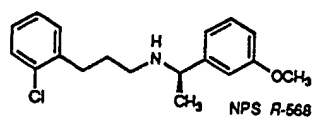
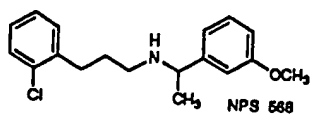
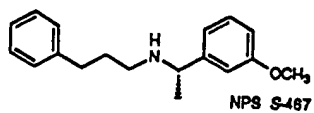
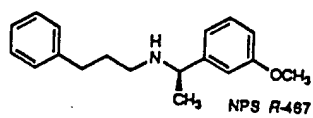
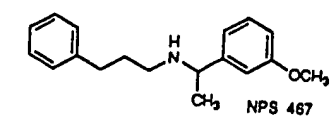


FIG. 36a.

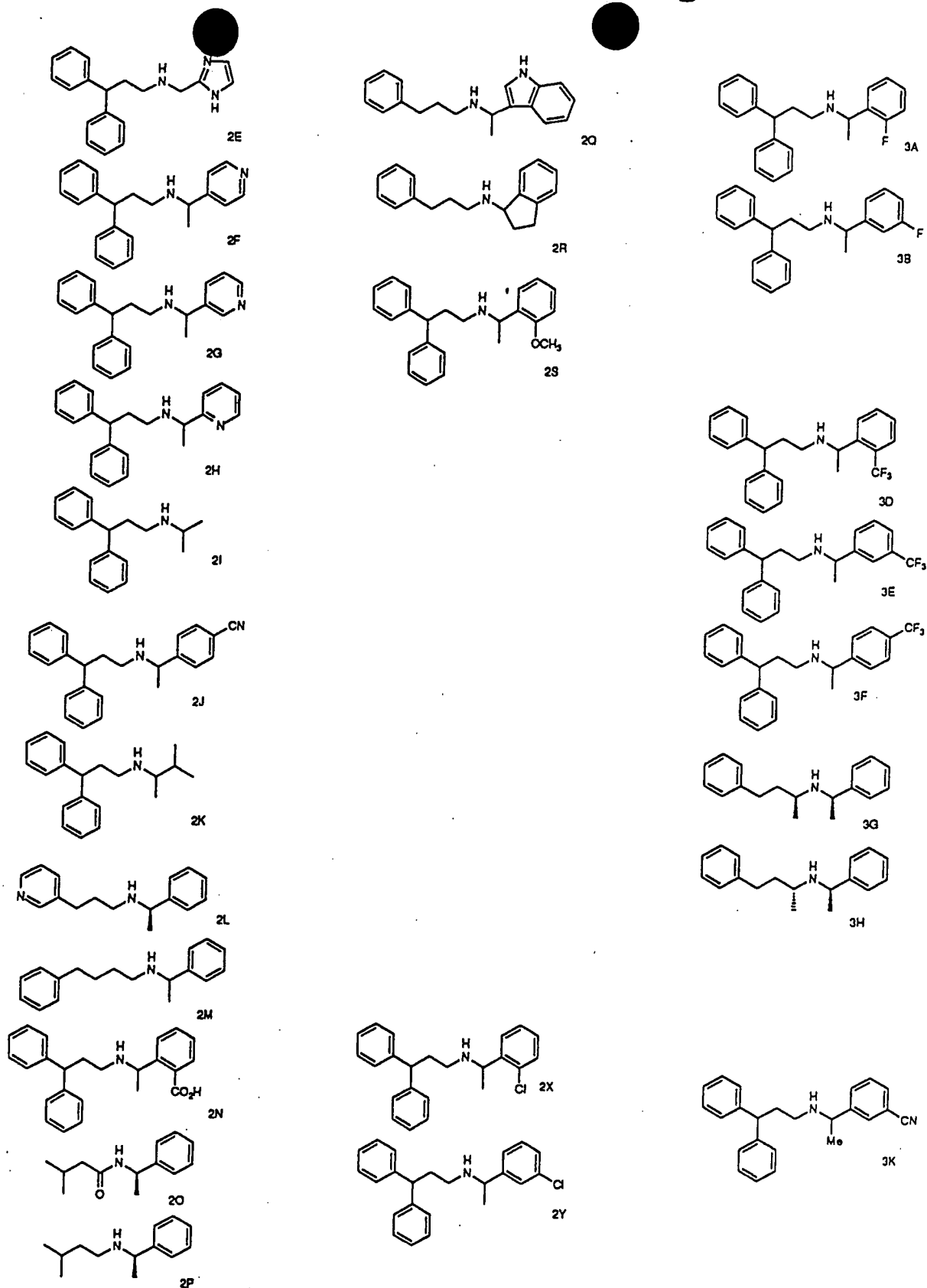


FIG. 36b.

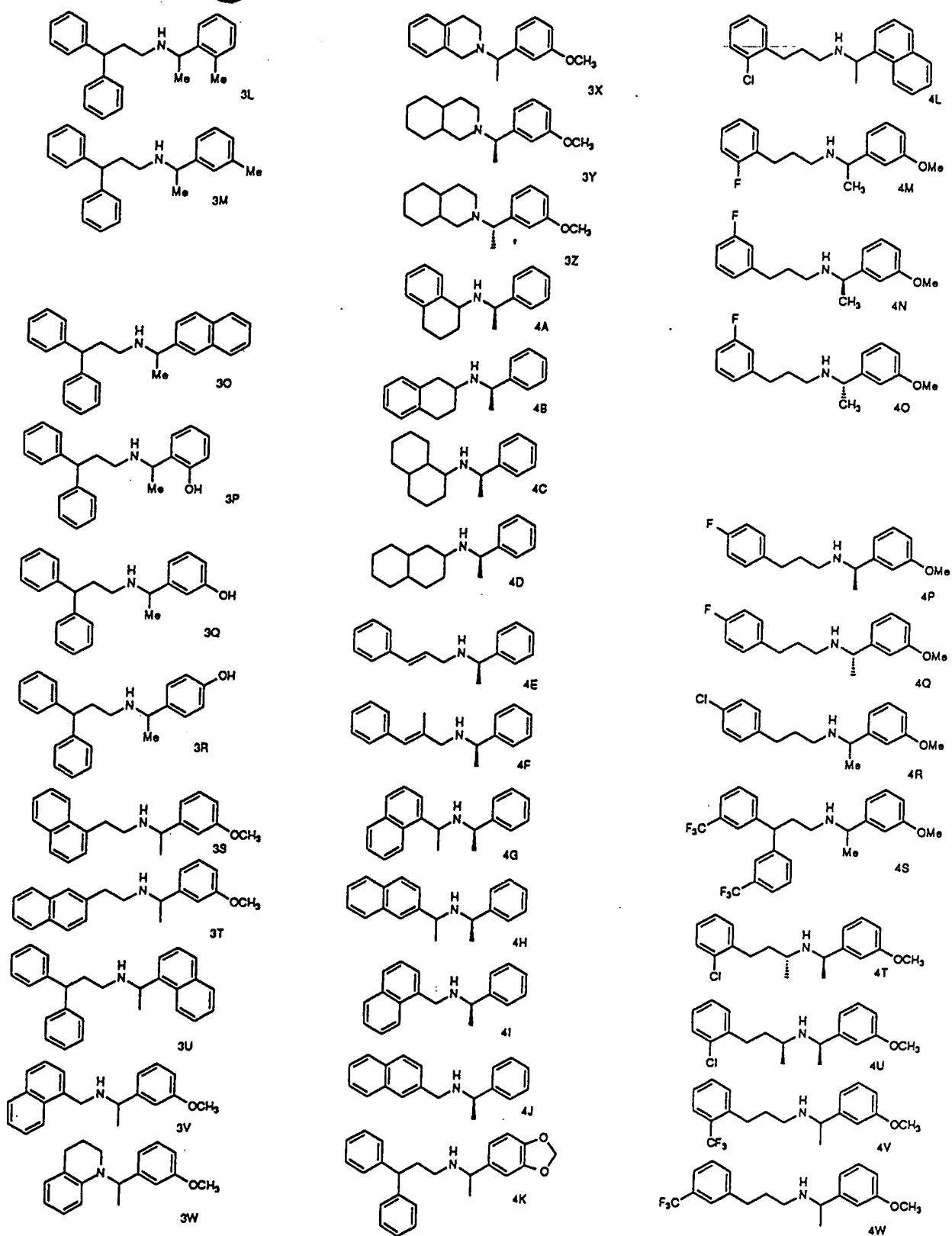


FIG. 36c.

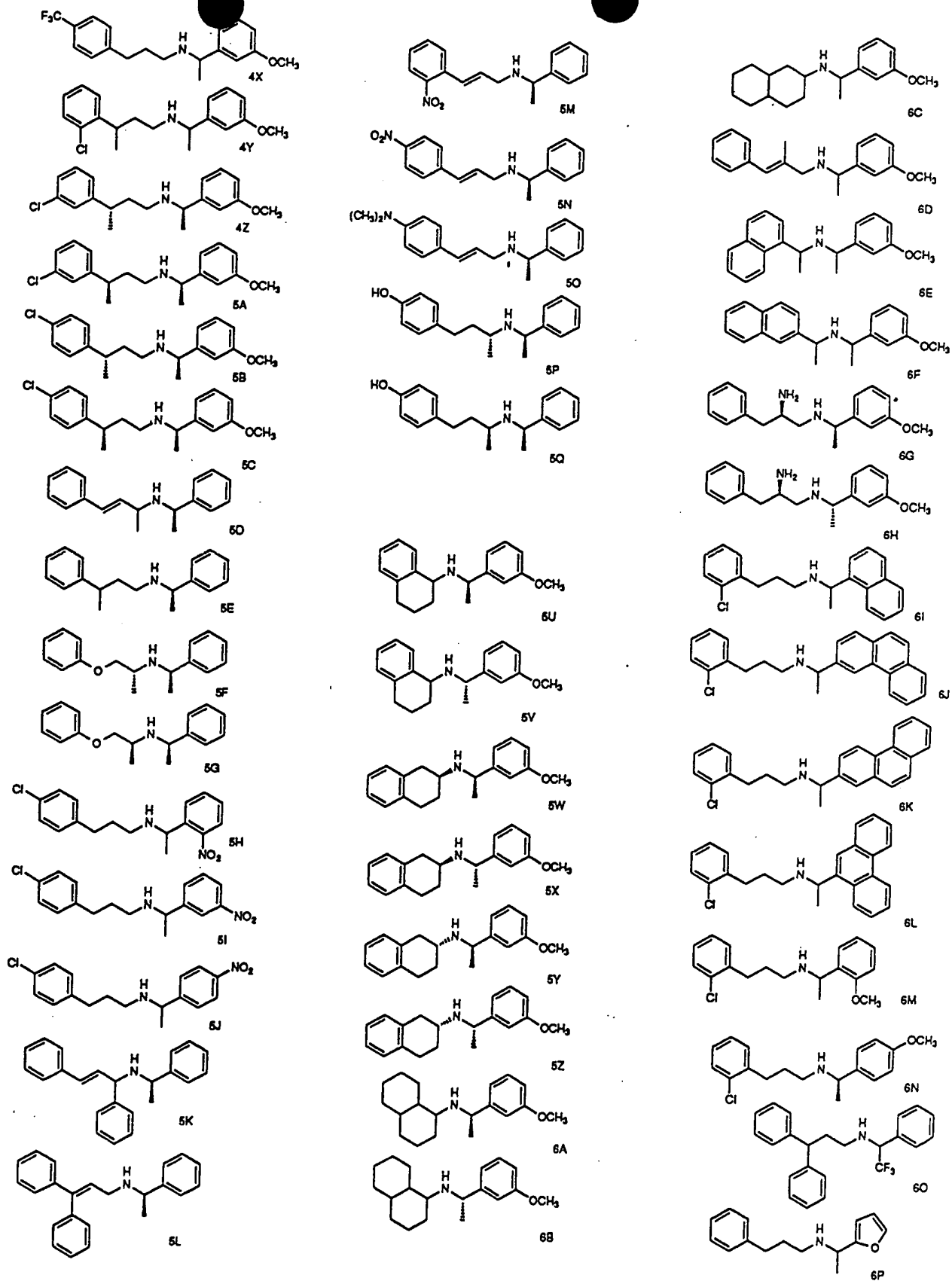


FIG. 36d.

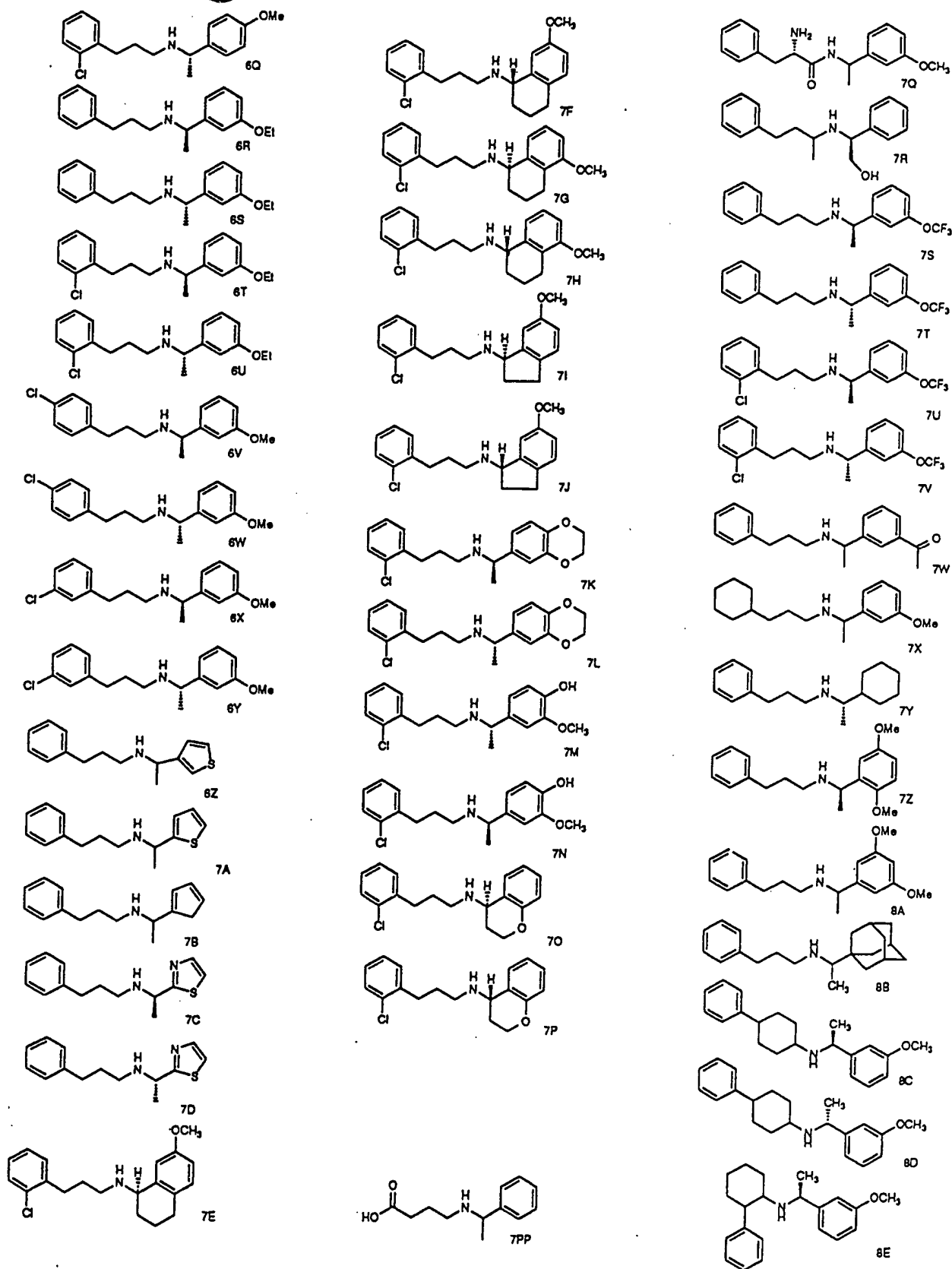


FIG. 36e.

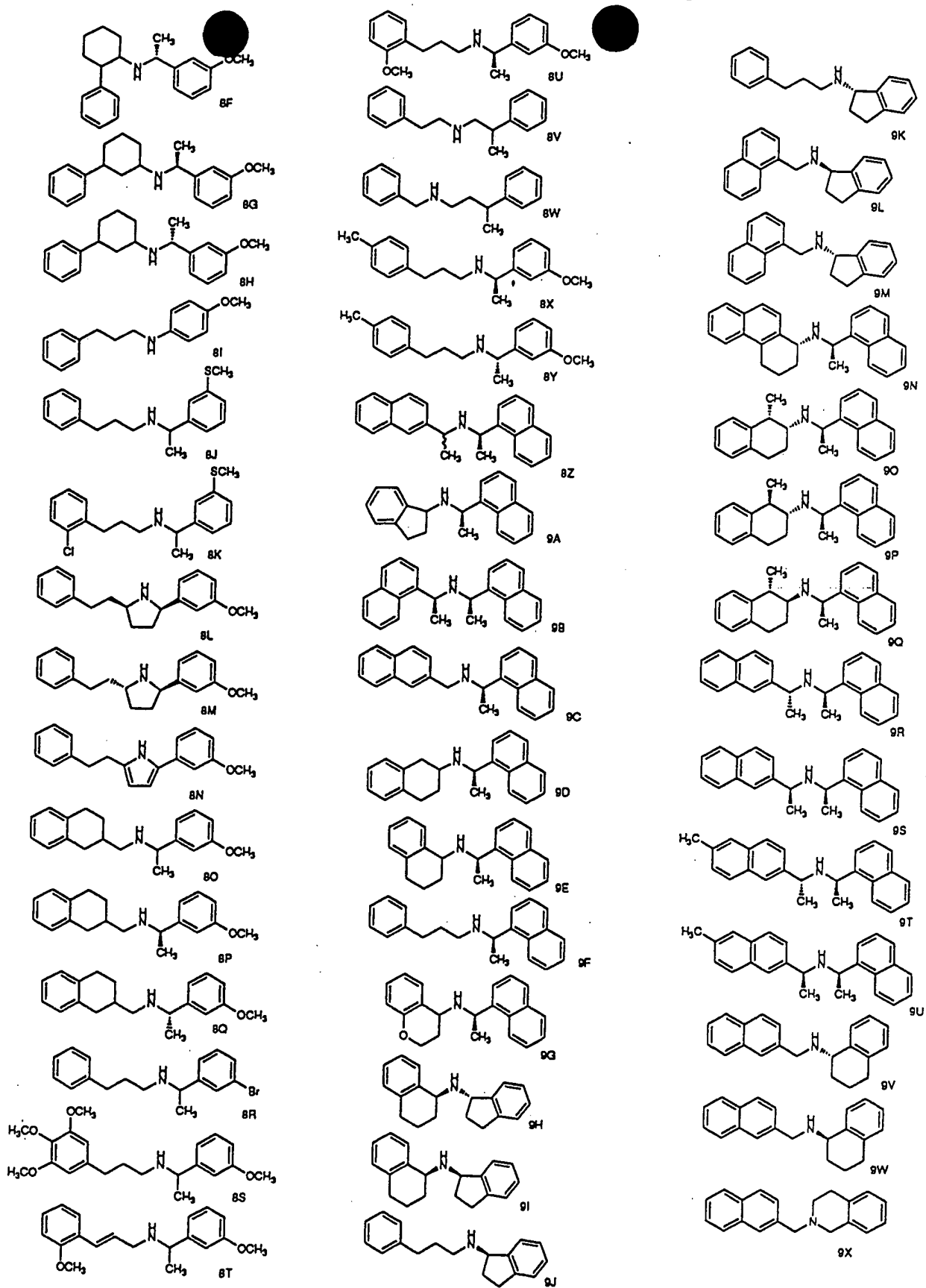


FIG. 36f.

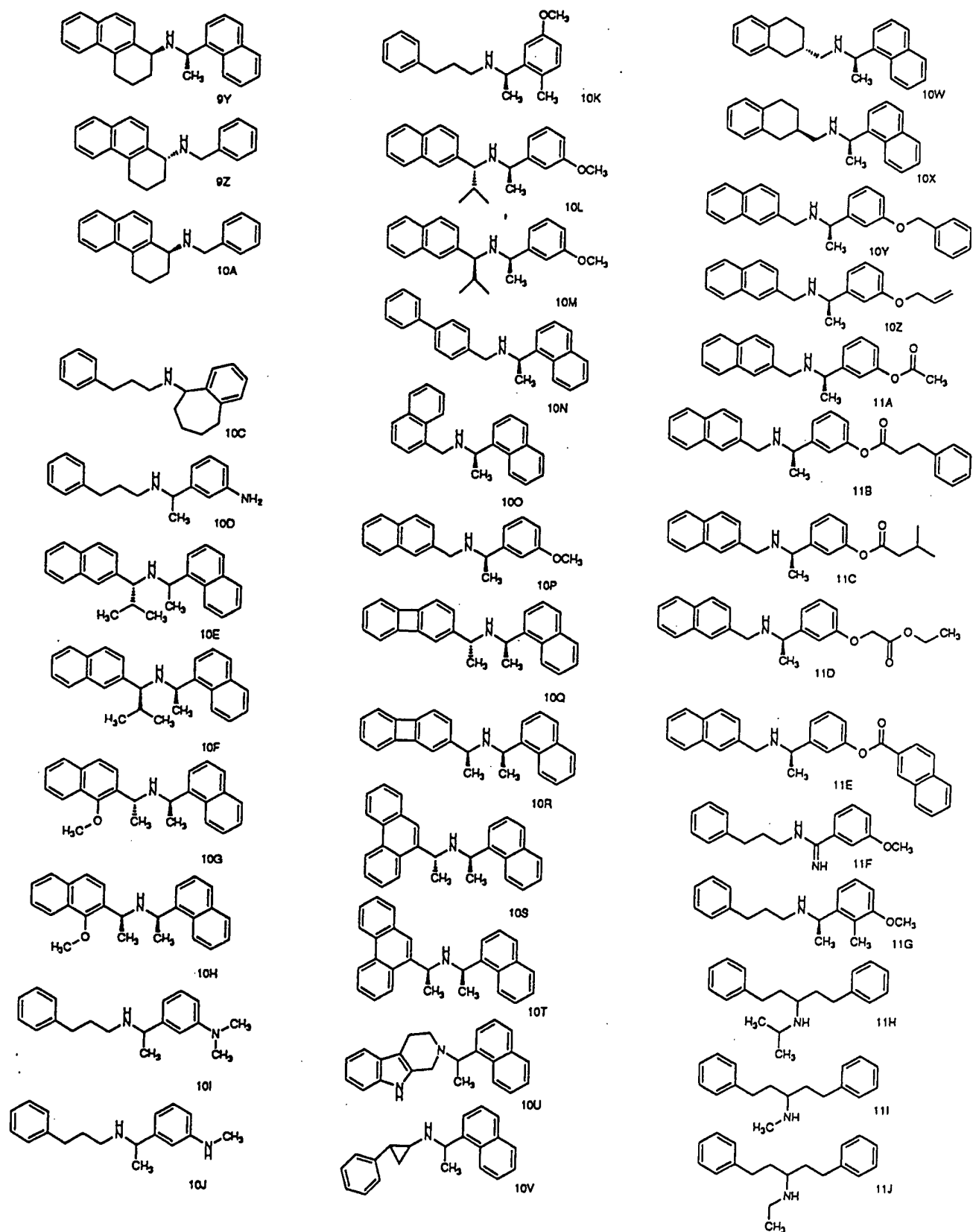


FIG. 36g.

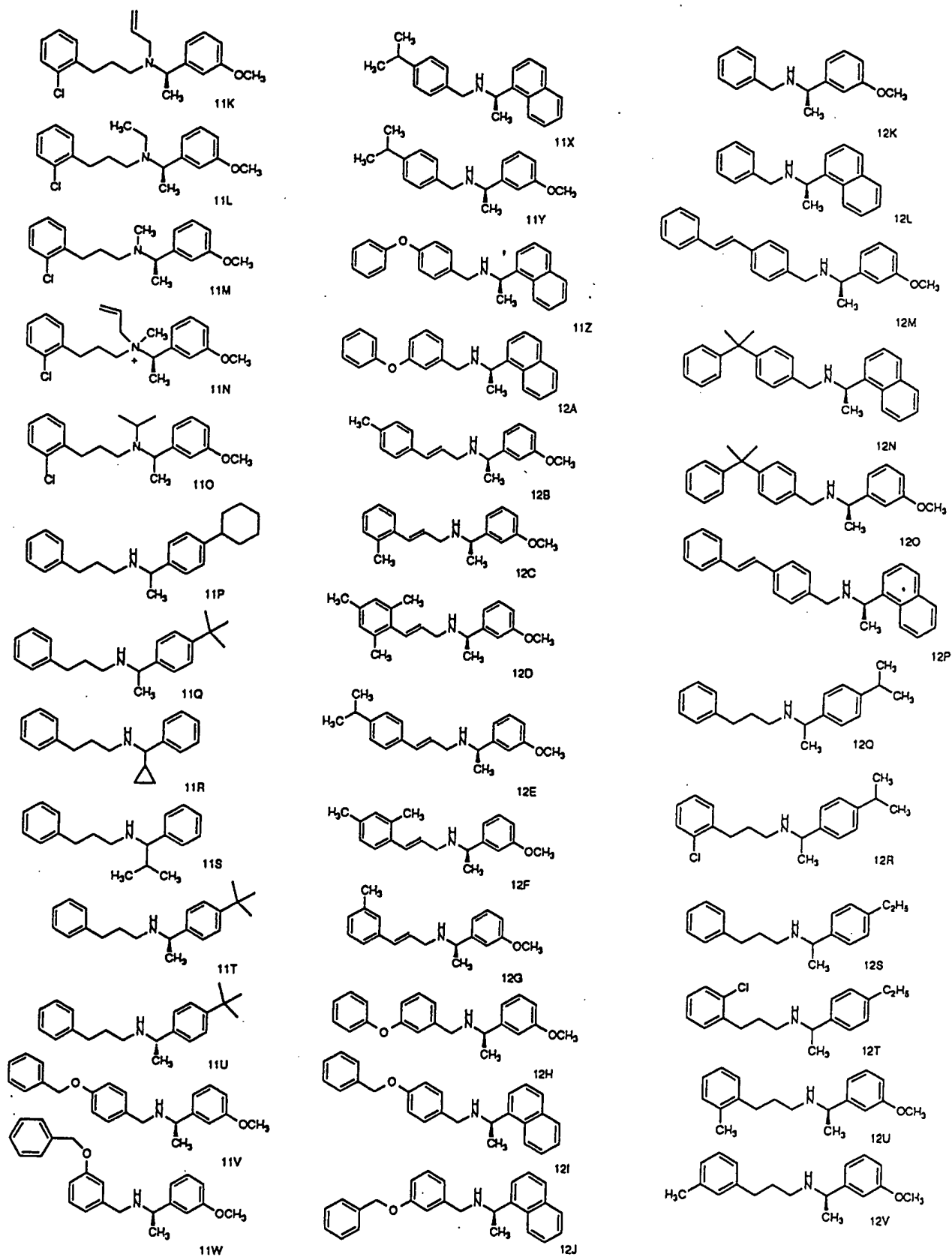


FIG. 36h.

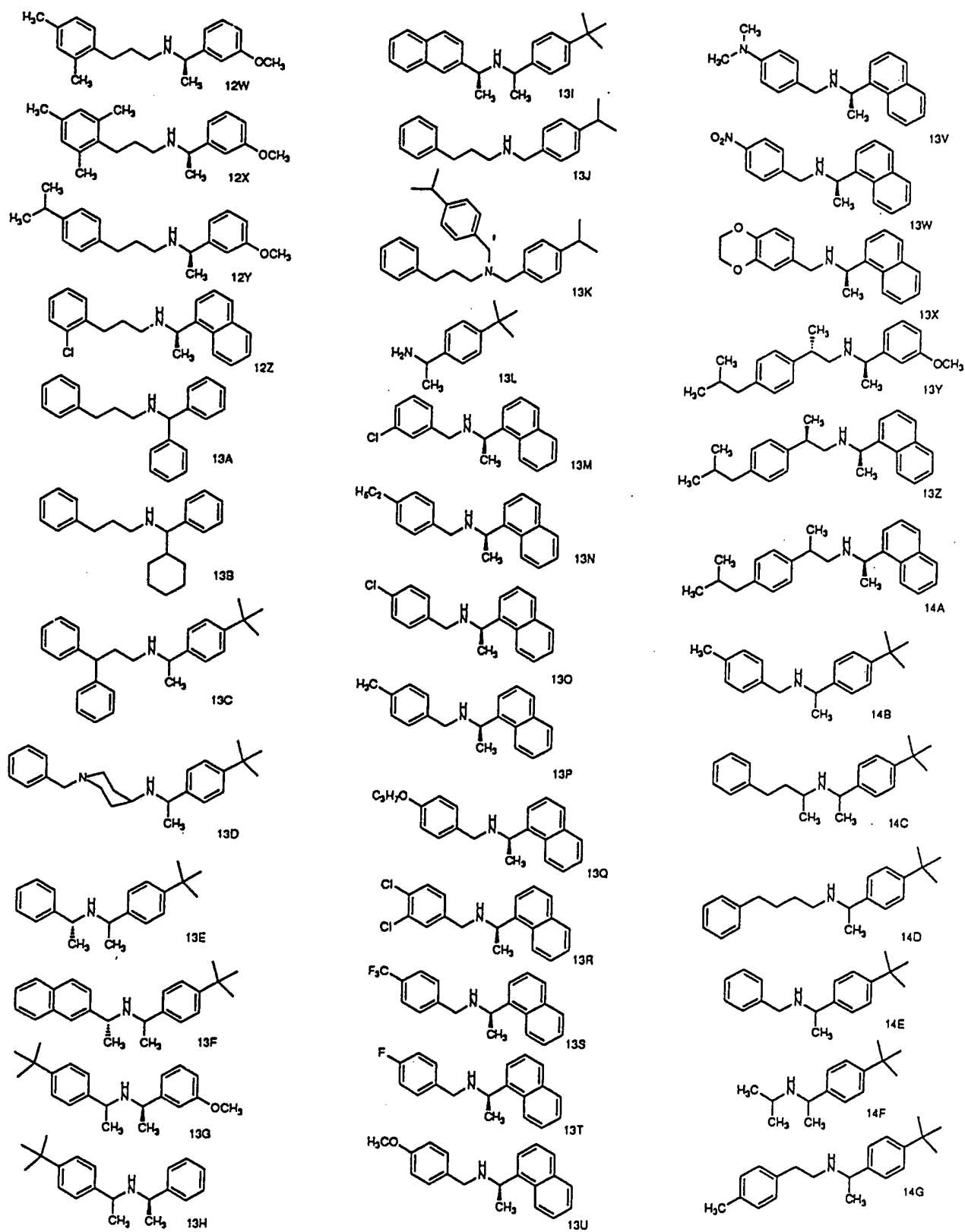


FIG. 36i.

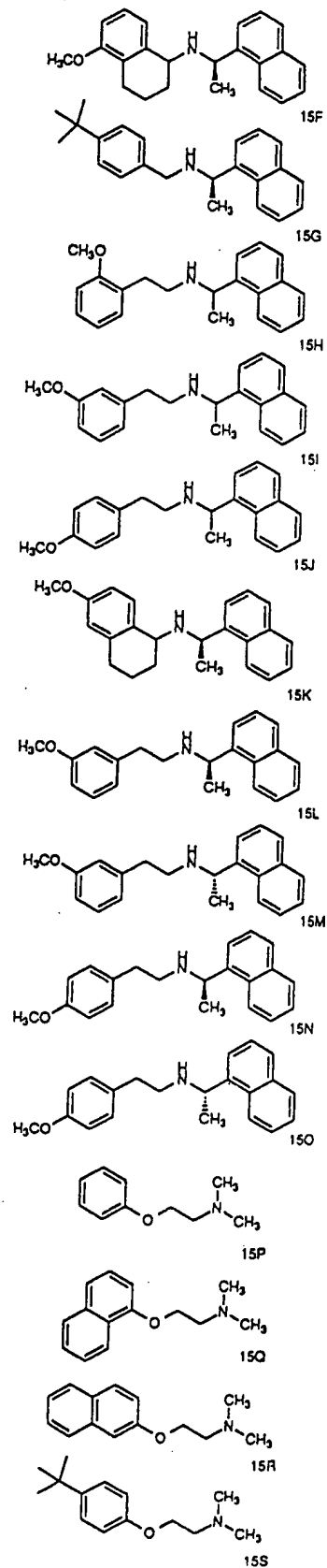
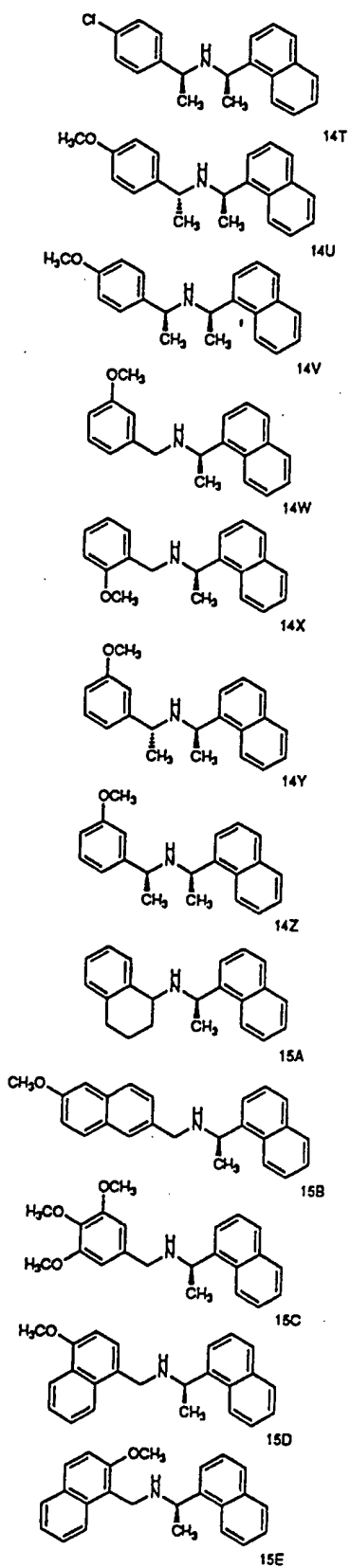
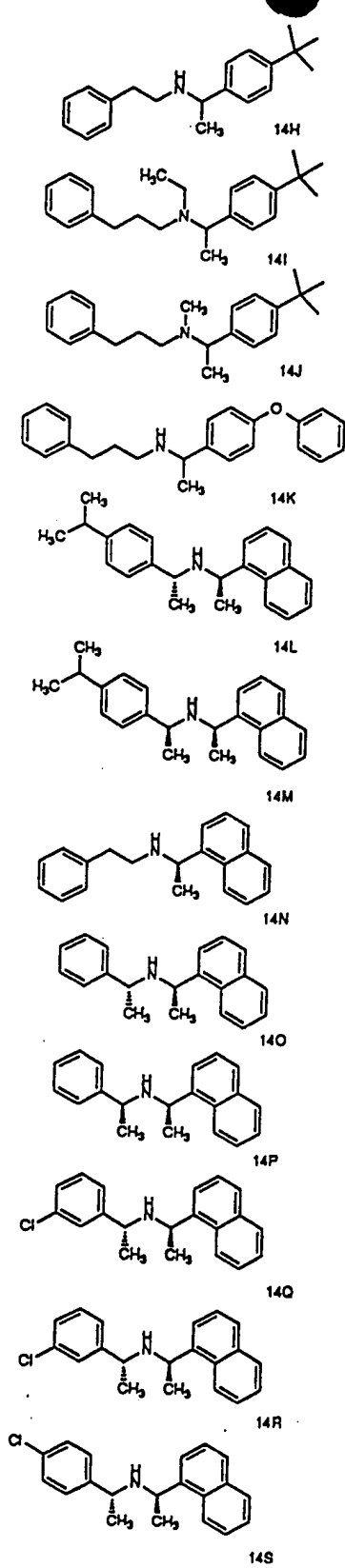


FIG. 36j.

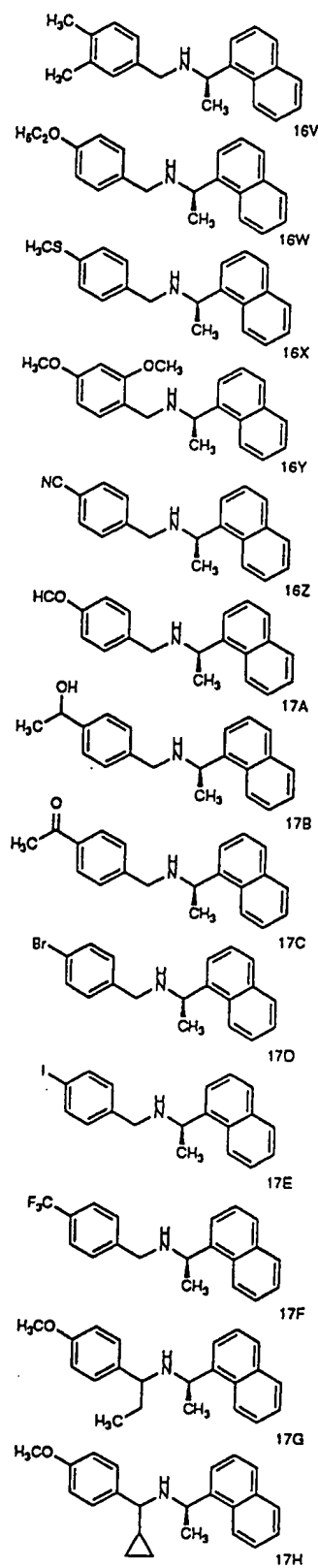
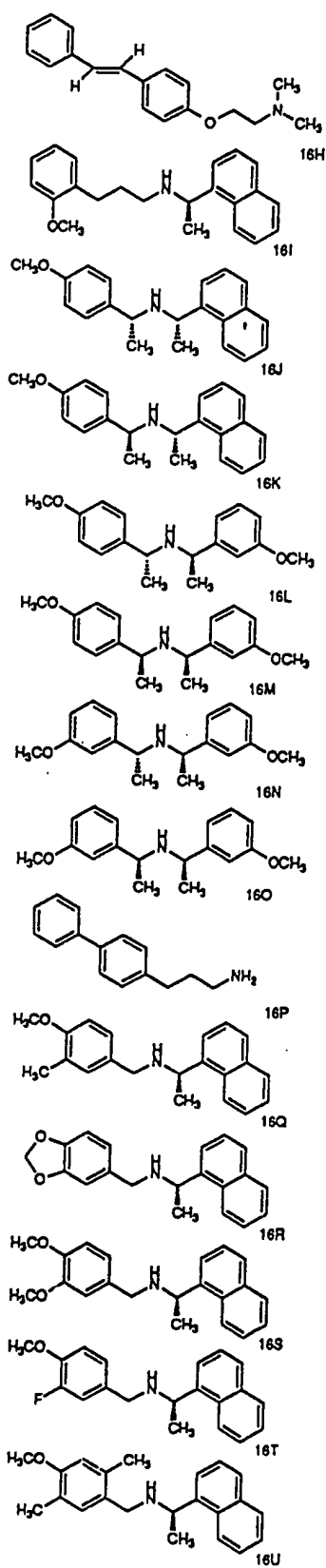
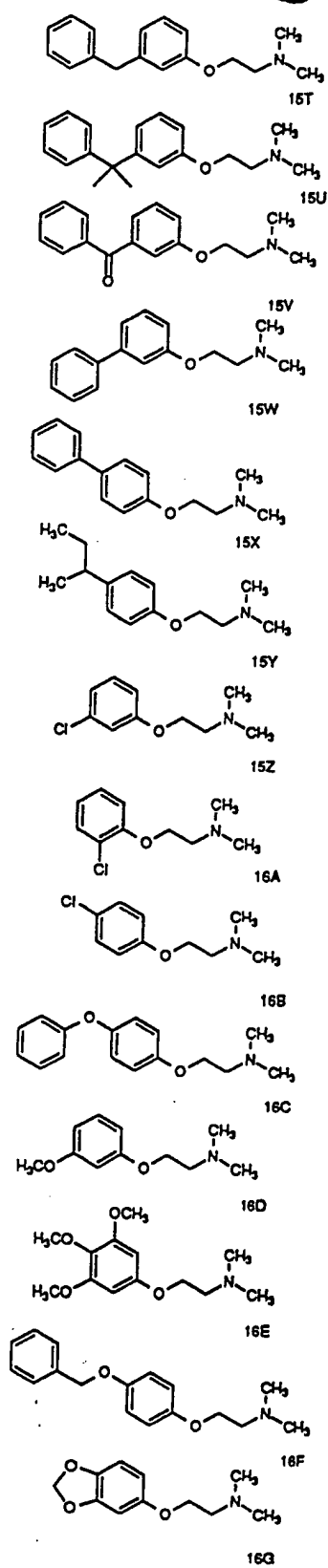


FIG. 36k.

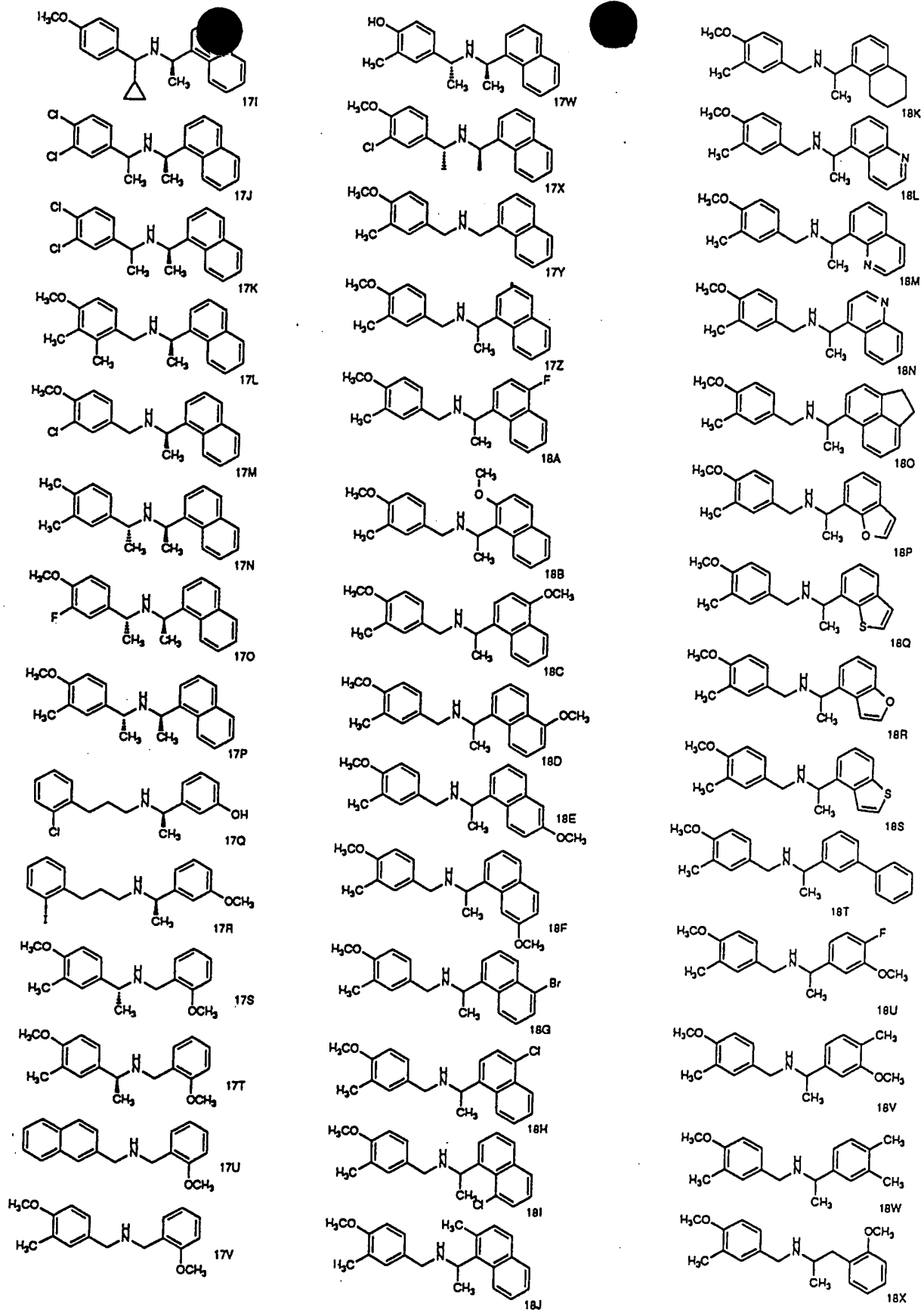


FIG. 361.

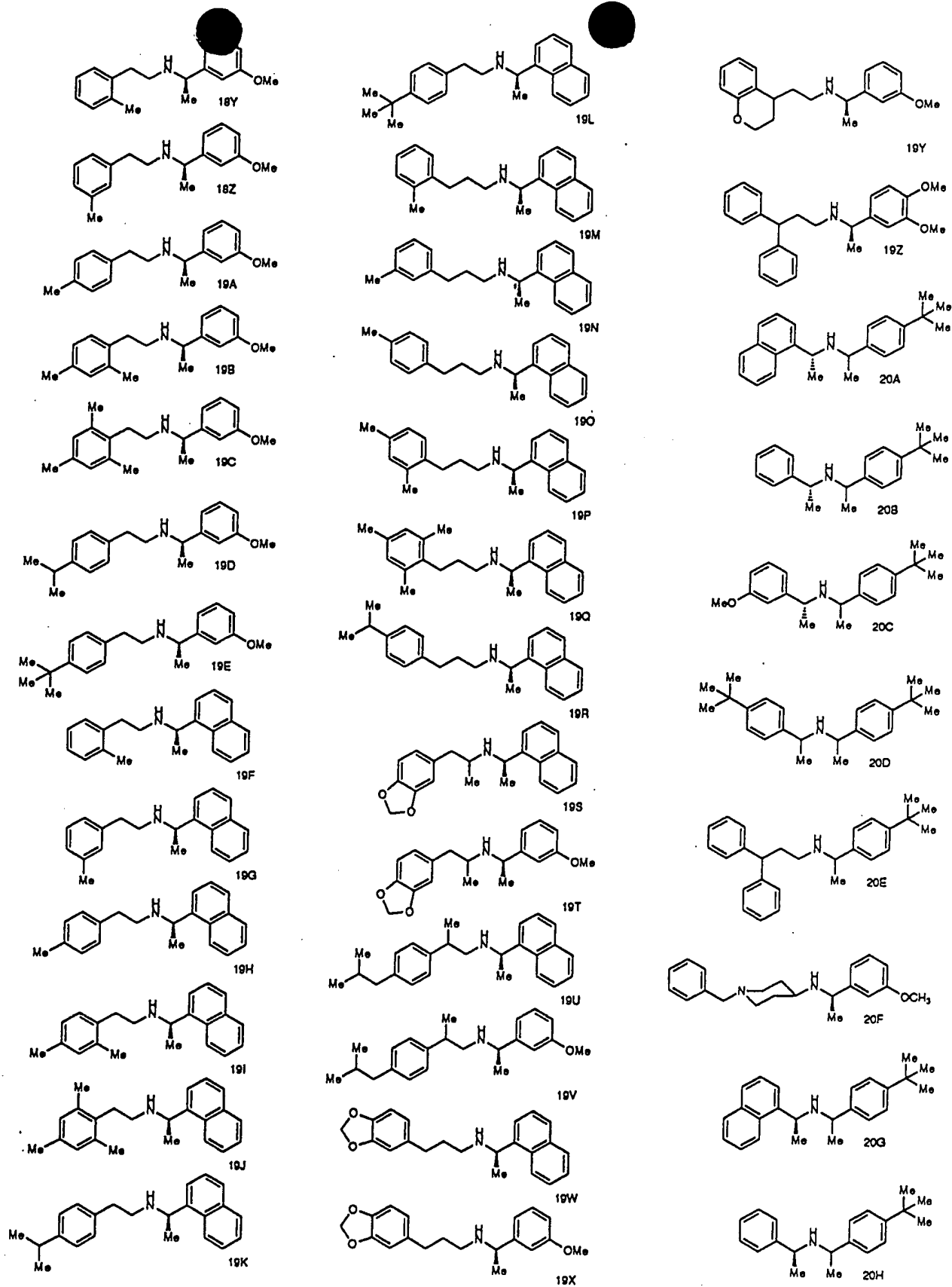


FIG. 36m.

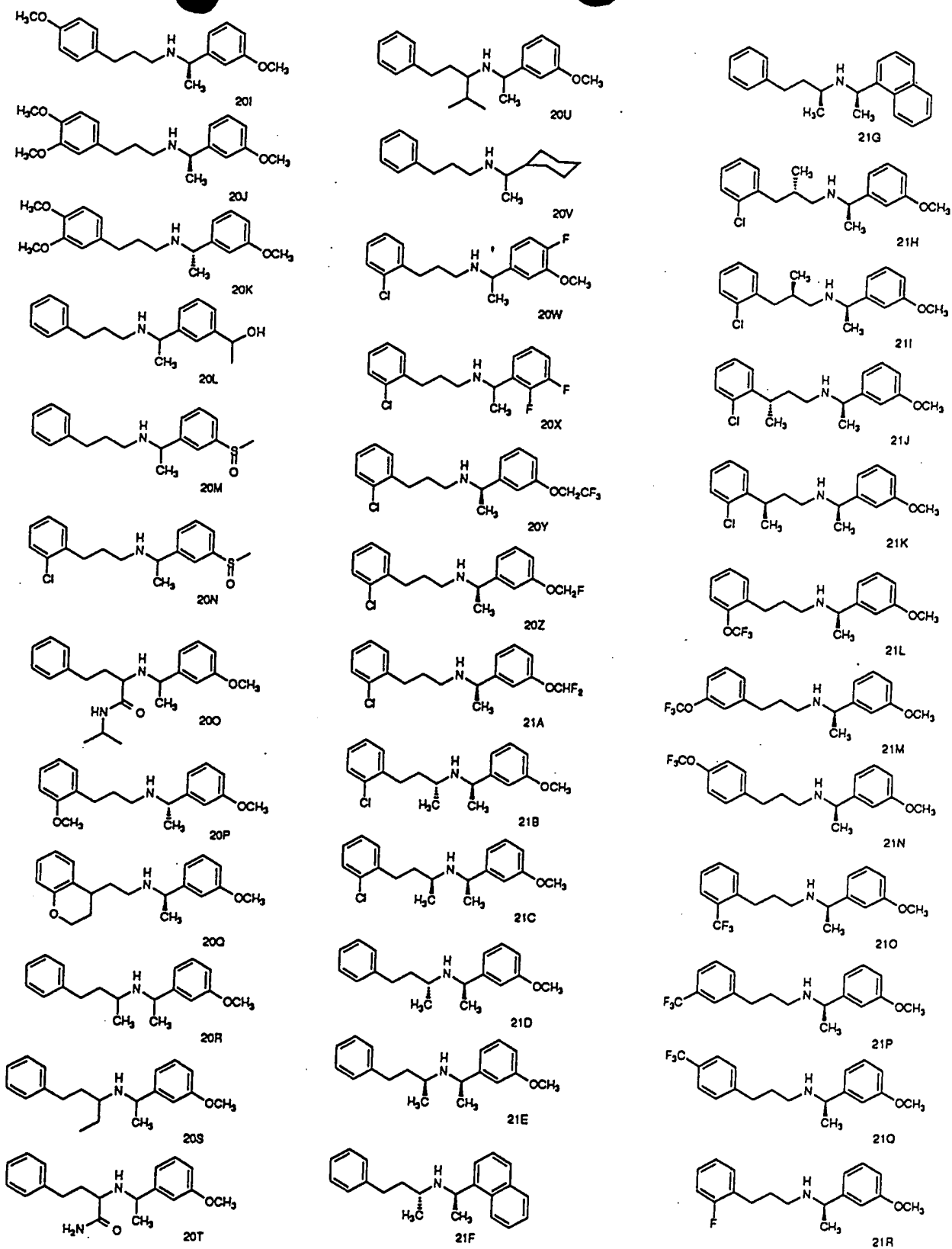


FIG. 36n.

FIG. 37a.

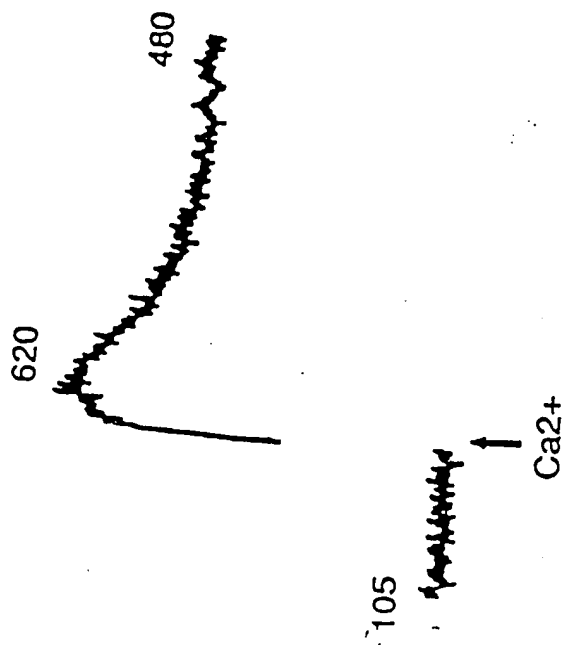
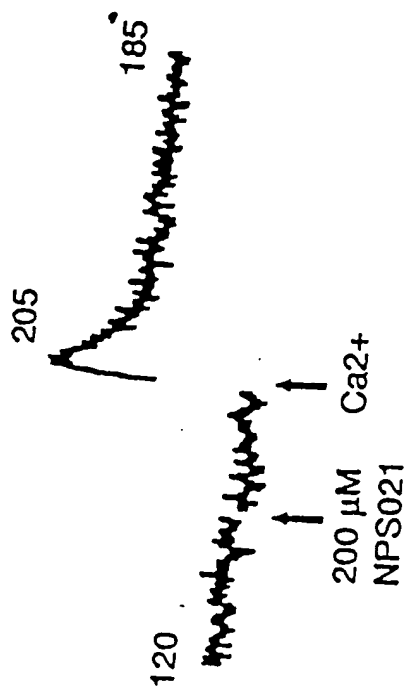
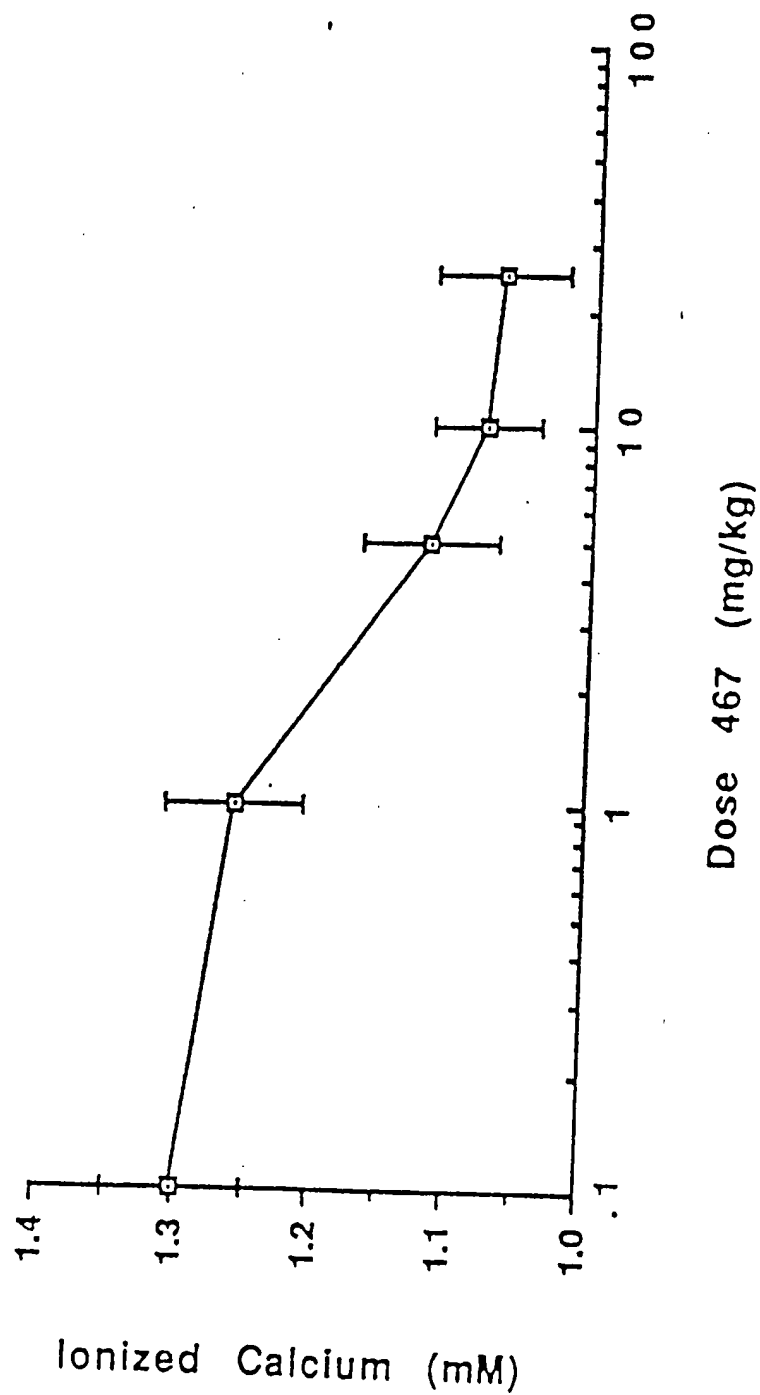


FIG. 37b.



Ionized Calcium Response to NPS 467



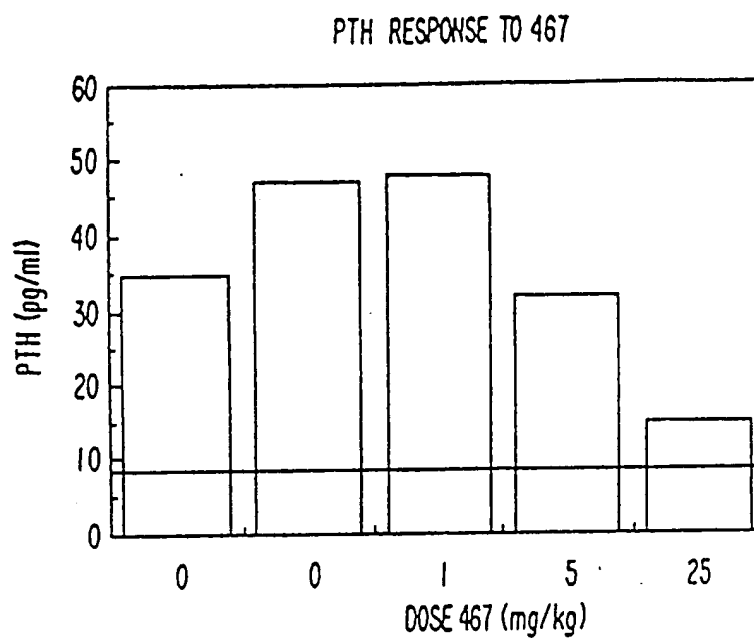


FIG. 39

FIG. 40.

Ionized Calcium Response to 25 mg/kg 467

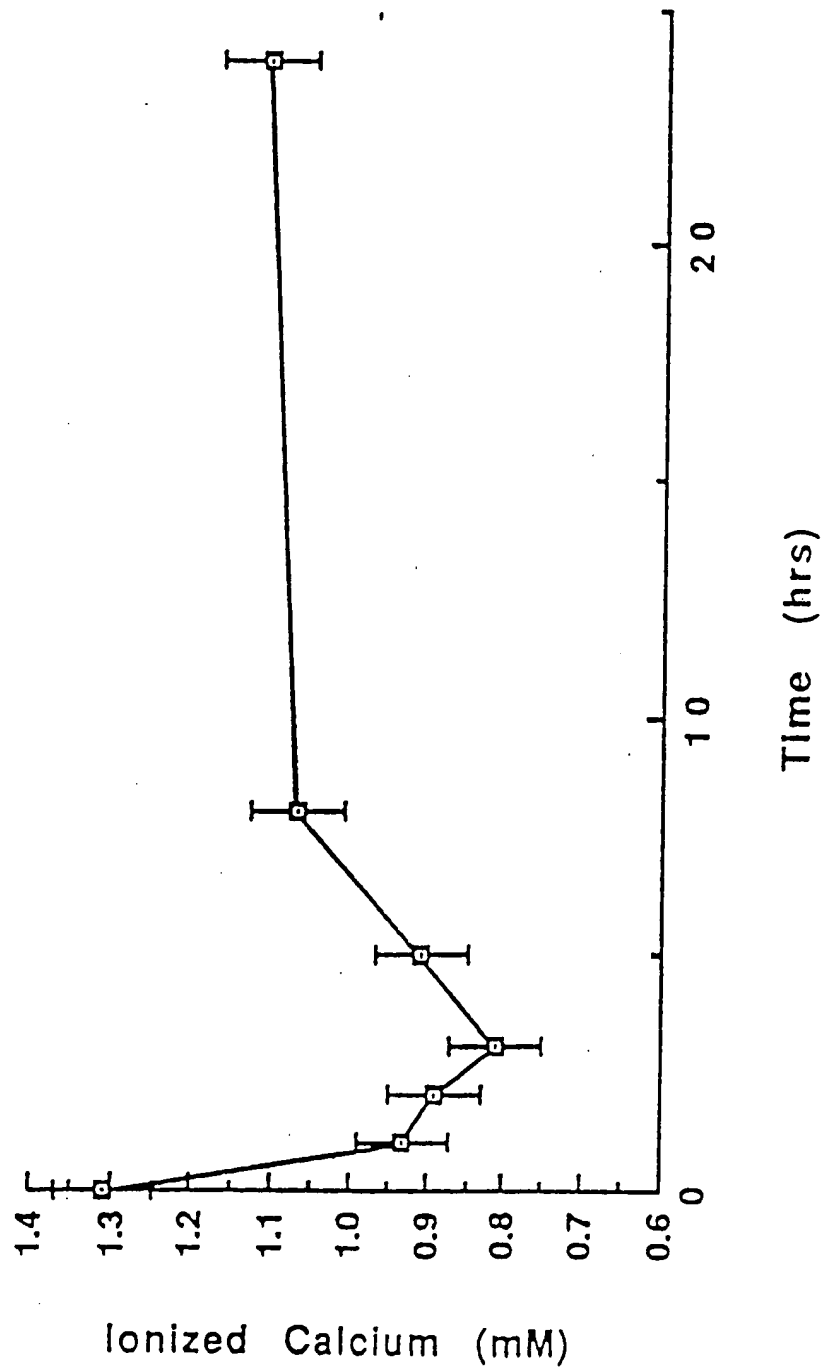
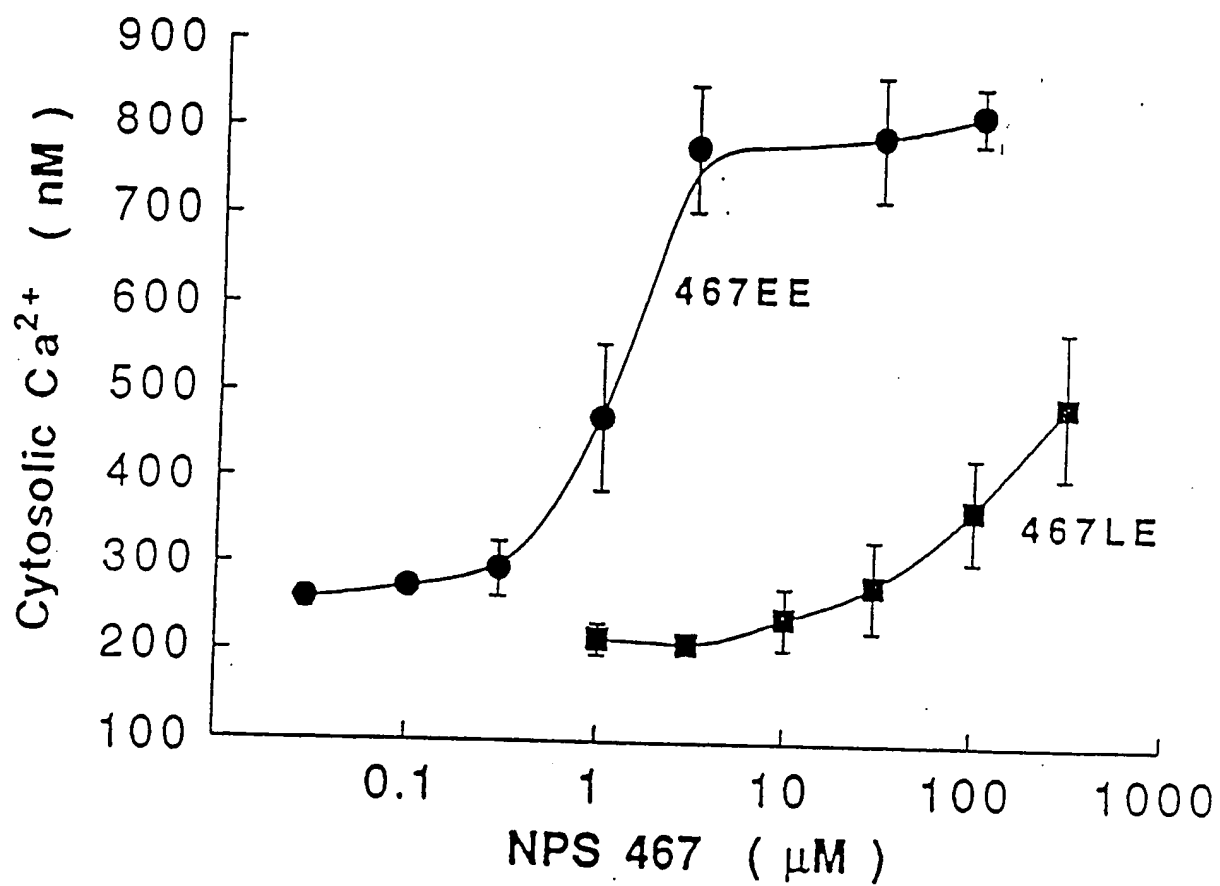


FIG. 41.



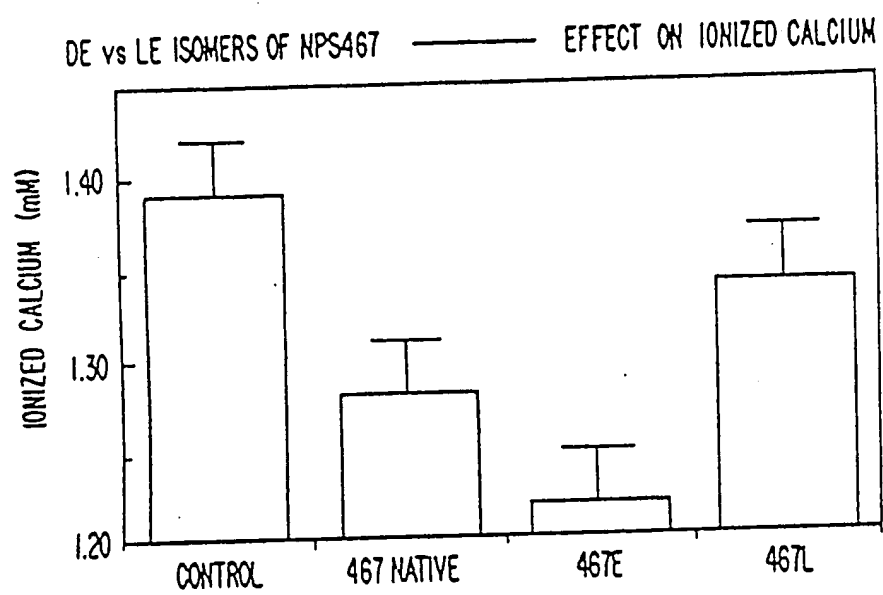
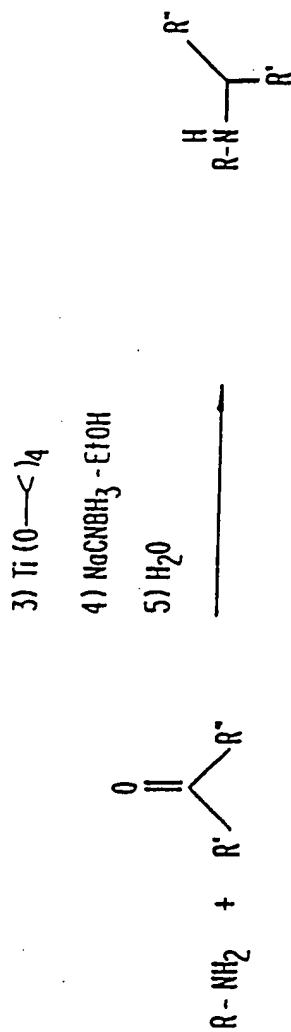


FIG. 42.

FIG. 43a.

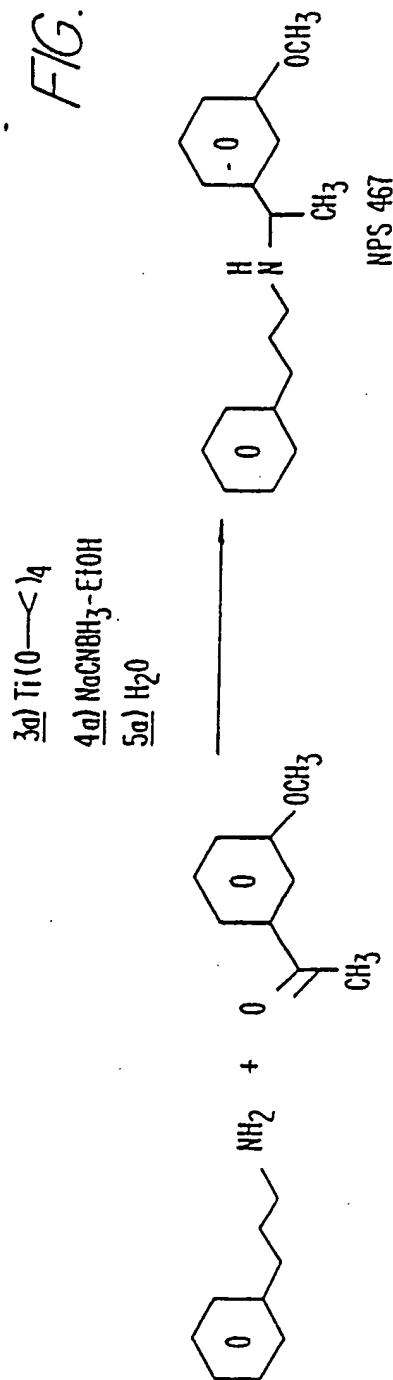


1

2

6

FIG. 43b.



1a

2a

6a

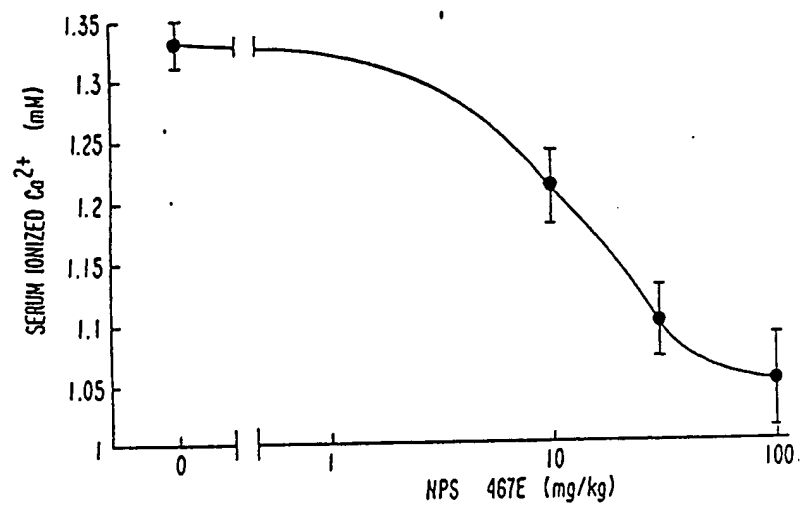


FIG. 44.

0750



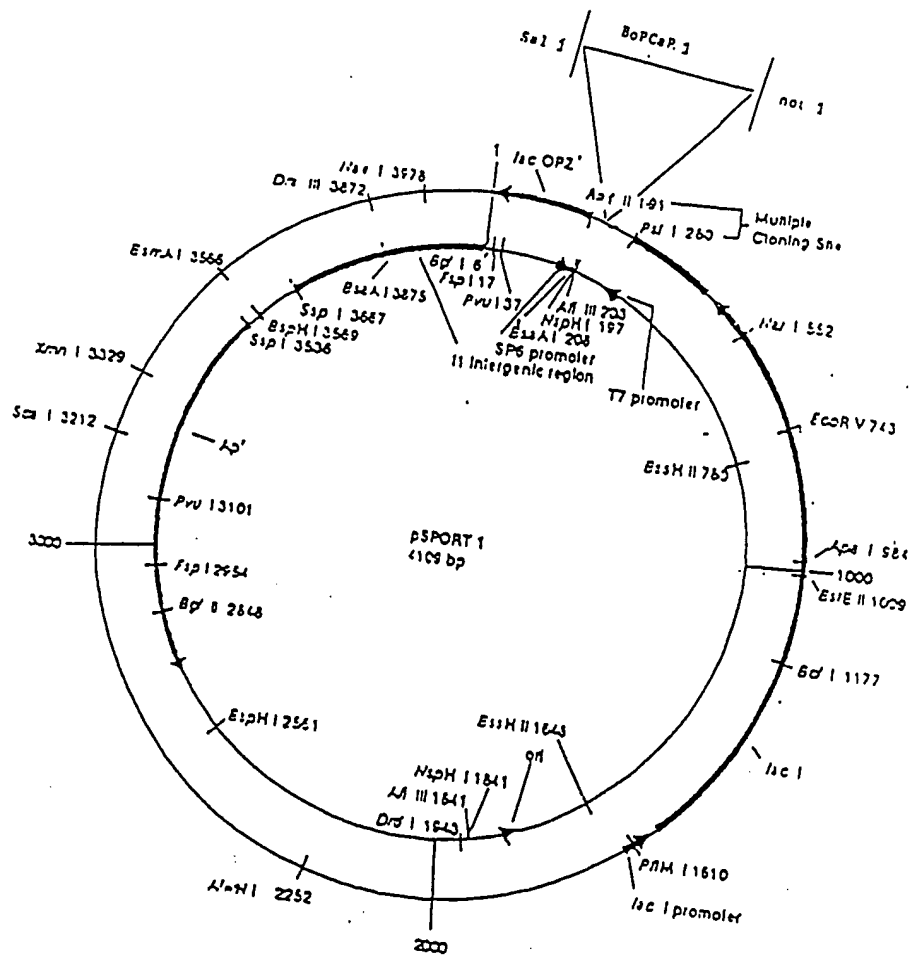


FIG. 46

pBoPCaR Sequence
(Seq. I.D. No. 1)

10	20	30	40	50	60	70	
12345678901234567890123456789012345678901234567890123456789012345							
CGGAAAAAAAAAAAAAGTTCCTCCACTCTAGTACAGAGAAGGTTGGCAGAGTCGTAAGCCCCAACCTCTAAACT							75
TCTCTGCATCTCCAAGGAGAAGGAGGGAAGAGGGGTTCTTTCCGACCTGAGGAGCTGGATCTGGGGTCCGAGAAC							150
CCCAAGGTAGCACCAGAAAGAACAGCACAGGAGGCGAGAGCGTGGCCGGTGGCCGGGAGAACAGACCCGACGCG							225
CGGTCTCGGCGCCGGGTCCCGGGGACTCAGCTCAGCAGGACTGGGAAGCCGAAAGTACTACACACGGTCTCTG							300
CATGATGTGACTTCTGAAGACTCAAGAGCCACCCACTTCACTAGTCTGCAATGGAGAAGGCAGAAATGAAAAGTC							375
AAACCCACGGTTCATTCTATTAATTCTGTAGACATGTCCCCCACTGCAGGGAGTGAGTCGCACCAAGGGGA							450
AGTCTCTCAGGGGCCCCCAGACCACCGCGCTTGAGTCCCTCTTCTGGAGAGAAAGCAGAACTATGGCACTTTA							525
						MetAlaLeuTy	
TAGCTGCTGTGGATCCTCTTGGCTTTTTCTACCTGGTGCACCTCCGCTATGGGCTGACCAGCGAGCCCAAAA							600
rSerCysCysTrpIleLeuLeuAlaPheSerThrTrpCysThrSerAlaTyrGlyProAspGlnArgAlaGlnLy							
GAAAGGGGACATTATCCTCGGGGGGCTCTTCTTCTATTCTTTGGGGTTGCAGTGAAAGATCAGGATCTAAAGTC							675
aLysGlyAspIleIleLeuGlyGlyLeuPheProIleHisPheGlyValAlaValLysAspGlnAspLeuLysSe							
GAGGCCGAGTCCGTGGAGTGTATCAGGTATAATTTCCGAGGATTTGCTGGTTACAAGCTATGATATTTGCCAT							750
rArgProGluSerValGluCysIleArgTyrAsnPheArgGlyPheArgTrpLeuGlnAlaMetIlePheAlaIle							
AGAGGAAATAAACAGCAGTCCAGCCCTCTTCCCAACATGACCCTGGGATACAGGATATTCGACACTTGAACAC							825
eGluGluIleAsnSerSerProAlaLeuLeuProAsnMetThrLeuGlyTyrArgIlePheAspThrCysAsnTh							
CGTCTCTAAAGCCTTGAGGGCCACCCTGAGTTTTGTGGCCAGAACAAATTGACTCTTTGAACCTTGATGAGTT							900
rValSerLysAlaLeuGluAlaThrLeuSerPheValAlaGlnAsnLysIleAspSerLeuAsnLeuAspGluPh							
CTGCACTGCTCAGAGCACATCCCTCTACCATCGCAGTGGTGGGAGCTACTGGCTCGGGCATCTCCACAGCAGT							975
eCysAsnCysSerGluHisIleProSerThrIleAlaValValGlyAlaThrGlySerGlyIleSerThrAlaVa							
GGCCAACCTGCTGGGGCTCTTCTACATCCCCAGGTCAGCTATGCCTCCCTCCAGCAGACTCTCAGCAACAAGAA							1050
IAIAsnLeuLeuGlyLeuPheTyrIleProGlnValSerTyrAlaSerSerSerArgLeuLeuSerAsnLysAs							
TCAATTCAAGTCCTTCTCCGCCACCATACCAATGATGAACACCAGGCCACGGCCATGGCTGACATCATCGAGTA							1125
nGlnPheLysSerPheLeuArgThrIleProAsnAspGluHisGlnAlaThrAlaMetAlaAspIleIleGluTy							
CTTCCGCTGGAAC TGGGTGGGCAACAATTGCAGCTGACGATGACTATGGCCGGCCAGGGATCGAGAAGTTTCGAGA							1200
rPheArgTrpAsnTrpValGlyThrIleAlaAlaAspAspAspTyrGlyArgProGlyIleGluLysPheArgGl							
GGAAGCTGAGGAGAGGGACATCTGCATCGACTTCAGCGAGCTCATCTCCAATACTCTGATGAGGAAAAGATCCA							1275
uGluAlaGluGluArgAspIleCysIleAspPheSerGluLeuIleSerGlnTyrSerAspGluGluLysIleGl							
GCAGGTGGTGGAGGTGATCCAGAATTCCACCGCCAAAGTCATTGTCTCTTCTCCAGCGGCCAGACCTGGAACC							1350
nGlnValValGluValIleGlnAsnSerThrAlaLysValIleValValPheSerSerGlyProAspLeuGluPr							
CCTCATCAAAGAGATCGTCCGGCGCAATATCACAGGCAGGATCTGGCTGGCCAGCGAGGCTGGGCCAGCTCTTC							1425
oLeuIleLysGluIleValArgArgAsnIleThrGlyArgIleTrpLeuAlaSerGluAlaTrpAlaSerSerSe							
CCTGATTGCTATGCCCGAGTATTTCCATGTGGTCCGAGGCACCATTTGGGTTTGGTTTGAAGCTGGGCAGATCCC							1500
rLeuIleAlaMetProGluTyrPheHisValValGlyGlyThrIleGlyPheGlyLeuLysAlaGlyGlnIlePr							
AGGCTTCCGGAAATTCCTGCAGAAAGTCCACCCAGGAAGTCTGTCCACAATGGTTTTGCCAAGGAGTTTTGGGA							1575
oGlyPheArgGluPheLeuGlnLysValHisProArgLysSerValHisAsnGlyPheAlaLysGluPheTrpGI							

FIG. 47a.

FIG. 47b.

10	20	30	40	50	60	70	
12345678901234567890123456789012345678901234567890123456789012345							
ACACGCCTTCAAGTGGCCGCGCCGAGCCACGCTGCGCCGCAGCAACGTCTCCCGCCAGCGGTCCAGCAGCCTAGG							3225
oHisAlaPheLysValAlaAlaArgAlaThrLeuArgArgSerAsnValSerArgGlnArgSerSerLeuGI							
GGGCTCCACGGGATCCACCCCTCTCTCCATCAGCAGCAAGAGCAACAGCGAGGACCCGTTCCTCAGCAGCA							3300
yGlySerThrGlySerThrProSerSerSerIleSerSerLysSerAsnSerGluAspProPheProGlnGlnI							
GCCGAAGAGGCAGAAGCAGCCGCGAGCCGCTGGCCCTGAGCCCGCACAAACGCGCAGCAGCCACAGCCGCGGCCACC							3375
nProLysArgGlnLysGlnProGlnProLeuAlaLeuSerProHisAsnAlaGlnGlnProGlnProArgProPr							
CTCGACCCACAGCCGCGACCCAGTCGAGCAGCGCCCGCGATGCAAGCAGAAGGTCATCTTCGGCAGCGGCAC							3450
oSerThrProGlnProGlnProGlnSerGlnGlnProProArgCysLysGlnLysValIlePheGlySerGlyTh							
CGTCACCTTCTCGTGAGCTTTGACGAGCCTCAGAAGACCGCGTGGCTCACAGGAATTCACGCACCAGACCTC							3525
rValThrPheSerLeuSerPheAspGluProGlnLysThrAlaValAlaHisArgAsnSerThrHisGlnThrSe							
CCTGGAGGCCAGAAAAACAATGACGCCCTGACCAACACAGGCGTTGCTCCCGTGCAGTGGGAGAGACGGA							3600
rLeuGluAlaGlnLysAsnAsnAspAlaLeuThrLysHisGlnAlaLeuLeuProLeuGlnCysGlyGluThrAs							
CTCAGAATTGACCTCCAGGAGACAGGCTGCAGGCGCTGTGGGTGAGGACCACAGCTAGAGATGGAGGACCC							3675
pSerGluLeuThrSerGlnGluThrGlyLeuGlnGlyProValGlyGluAspHisGlnLeuGluMetGluAspPr							
CGAAGAGATGTCCCGGCCTTGTAGTGTCTAATTCGCGAGCTTTGTCTCAGTGGCGGAGGCAGCACTGTTAC							3750
oGluGluMetSerProAlaLeuValValSerAsnSerArgSerPheValIleSerGlyGlyGlySerThrValTh							
GGAAAACATGCTGCGTTCTTAAAGGGAAGGAGAAAGCCAGTTCAGGGGGAATCCAGGCAGTTTCCCGGGGATGA							3825
rGluAsnMetLeuArgSer							
CCTTCTCCAAAGGGATGAGGAAGTGCCTCCCAACCCCAACCCCTTCTCCAGGAAGGAGGGATAAGACCCACCA							3900
AATGCTTGAACCTTAGTTGCACTGCTATAAACGACAGTGAATGAAATAATGTCCCCCTTAAATTAAGAGGG							3975
GAGCGGTGTGCTTCTGTGGTTAGGTTTATCAGAGTGCTGAGATCCCTATAGTCAGGTTGCGCTTCTATCCCTG							4050
CTTCCATTCTCCTTCTGTCTATCCCATCCAACAGTCCAGAGATAAAACCATGGCTTTAAGATACCCACCTAT							4125
TCCCCCTAGGGTCTTATTTGTTGTTTTGTTGCTGTTGTTTTGGTTTGATTTTGTTTTAAATGTTGAAACGTCT							4200
GCCCTGAACCTTTCAGACAGCCTGGTCCAAAAACAACTGTGCAGAGTGACAGGACCTCCTATGGGCACCACTA							4275
GAGTTGAGTGCGAAAGACAGAATGTGCCAGCGCTGCCAACACCTTGACAGTGGGAAGAAGCTTGAAATGTCCAG							4350
AGCTGTAAGATGAATGTGTCCCTCCTATTTATGAAAAATGTTAAATATGTGGTTTCTACTTGCTGCTGCTGTC							4425
ACGTGACATGGAGAAGGTTAGCATCCATCCTCCAGCAGTATGTCTGATCTTGTCAGAGTGTGATGGTGATGCCA							4500
CGTTTAGATTCCAATATCTCAGGAATCACCTCAGCCTGCATGAATCCAATGAGCTGTATCTGTAATTAATATTGT							4575
CATATGTAGCTTTATCCTTAAGAAAAATGTGTTTGTGTTTAAATAGTCCGTGGAAAAATATAAGCTGGAAAAATGTCC							4650
CAGTCTGGTTGATATAAGGCAGTATTATTGAGTCCCGTTTTCTTTGCCCGCCCCACCACCCACACCCCAATGAGC							4725

FIG. 47c.

pBoPCaR Sequences

10	20	30	40	50	60	70	
12345678901234567890123456789012345678901234567890123456789012345							
TAAGCCCTAAATGAGCCCTTTCAGGGCCAGGGATCCAGAAGCTCCCTCTTCTCCACCCCAACGCTTCCTGAA							4800
GTCAGATCCATGCCTTTCCTGTGAAGAATAAGCTCCAGTCTCTGACCTCTACCAGTTTCTGGGGTAAGAACA							4875
CGTGGTTCCAAGAGAGCTCTCATGGGATATTACTCTTGGCACCCCCCAATGCCATACTTAGGTTCCCTCCAGCAG							4950
TGGGATCTGCCCATGGGTAGTTACAAGATTGAACGTTGAATGGCATACTGCTGAACAGTCAGTTCTGGAGCTAGA							5025
GAGGCCTGGGGTCAAGTGCTGGGTTTGTCACTCACAAGTTGGGTGACCACAGGCAGGGAACCTTGACCTCACTCA							5100
GCCCCAGCTTCTTTGTGTCTAAAATGGAGGTAATAATCATCCTTTTCCCGCAGAGCTCTTATGTGGGTAAATGA							5175
GATAAATGTATGTAAAGTATTTAGCATGGTGCCTAGCCCATAGTAAGCACGCAATAAATATTAGTTAATATTAA							5250
AAAAAAAAAAAAAAAAAAAAAAAAAAAA							5275

FIG. 47d.

pHuPCaR5.2 Sequence

(Seq. I.D. No. 2)

10	20	30	40	50	60	70	
12345678901234567890123456789012345678901234567890123456789012345							
GCTGCTGTGGCCGGACCCGAAGCGGGCGCCGGGAGCGCAGCGAGCCAGACGCGCCTCTCCAAGACCGTGACCTT							75
GGCATAGGGAGCGGGGCTGCGCGCAGTCCTGAGATCAGACCAGAGCTCATCTCGTGGAGACCCACGGCCGAGGG							150
GCCGGAGCTGCCTCTGTGCGAGGGAGCCCTGGCCGCGGCGCAGAAGGCATCACAGGAGGCCTCTGCATGATGTGG							225
CTTCCAAAGACTCAAGGACCACCCACATTACAAGTCTGGATTGAGGAAGGCAGAAATGGAGATTCAAACACCACG							300
TCTTCTATTATTTTATTAATCAATCTGTAGACATGTGTCCCACTGCAGGGAGTGAAGTCTCTCCAAGGGAGAAAC							375
TTCTGGGAGCCTCCAAACTCCTAGCTGTCTCATCCCTTGCCCTGGAGAGACGGCAGAACCATTGGCATTATATAGC							450
						MetAlaPheTyrSer	
TGCTGCTGGGTCTCTTGGCACTCACCTGGCACACCTCTGCCTACGGGCCAGACCAGCGAGCCAAAAGAAGGGG							525
CysCysTrpValLeuLeuAlaLeuThrTrpHisThrSerAlaTyrGlyProAspGlnArgAlaGlnLysLysGly							
GACATTATCCTTGGGGGGCTCTTCTTATTCATTTGGAGTAGCAGCTAAAGATCAAGATCTCAAATCAAGGCCG							600
AspIleIleLeuGlyGlyLeuPheProIleHisPheGlyValAlaAlaLysAspGlnAspLeuLysSerArgPro							
GAGTCTGTGGAATGTATCAGGTATAATTTCCGTGGGTTTCGCTGGTTACAGGCTATGATATTTGCCATAGAGGAG							675
GluSerValGluCysIleArgTyrAsnPheArgGlyPheArgTrpLeuGlnAlaMetIlePheAlaIleGluGlu							
ATAACAGCAGCCAGCCCTTCTTCCAACTTGACGCTGGGATACAGGATATTTGACACTTGCAACACCGTTTCT							750
IleAsnSerSerProAlaLeuLeuProAsnLeuThrLeuGlyTyrArgIlePheAspThrCysAsnThrValSer							
AAGGCCCTTGAAGCCACCCTGAGTTTTGTGCTCAAACAAAATTGATTCTTTGAACCTTGATGAGTTCTGCAAC							825
LysAlaLeuGluAlaThrLeuSerPheValAlaGlnAsnLysIleAspSerLeuAsnLeuAspGluPheCysAsn							
TGCTCAGAGCACATTCCCTCTACGATTGCTGTGGTGGGAGCAACTGGCTCAGGCGTCTCCACGGCAGTGGCAAT							900
CysSerGluHisIleProSerThrIleAlaValValGlyAlaThrGlySerGlyValSerThrAlaValAlaAsn							
CTGCTGGGGCTCTTCTACATTCCCAAGTCACTTATGCCTCTCCAGCAGACTCTCAGCAACAAGAATCAATTC							975
LeuLeuGlyLeuPheTyrIleProGlnValSerTyrAlaSerSerSerArgLeuLeuSerAsnLysAsnGlnPhe							
AAGTCTTCTCCGAACCATCCCAATGATGAGCACCAGGCCACTGCCATGGCAGACATCATCGAGTATTTCCGC							1050
LysSerPheLeuArgThrIleProAsnAspGluHisGlnAlaThrAlaMetAlaAspIleIleGluTyrPheArg							
TGGAAGTGGGTGGGCACAATTGCAGCTGATGACGACTATGGGCGGCCGGGGATTGAGAAATCCGAGAGGAAGCT							1125
TrpAsnTrpValGlyThrIleAlaAlaAspAspAspTyrGlyArgProGlyIleGluLysPheArgGluGluAla							
GAGGAAAGGGATATCTGCATCGACTTCAGTGAACCTCATCTCCAGTACTCTGATGAGGAAGAGATCCAGCATGTG							1200
GluGluArgAspIleCysIleAspPheSerGluLeuIleSerGlnTyrSerAspGluGluGluIleGlnHisVal							
GTAGAGGTGATTCAAAATTCACGGCCAAGTCACTCGTGGTTTTCTCCAGTGGCCAGATCTTGAGCCCTCATC							1275
ValGluValIleGlnAsnSerThrAlaLysValIleValValPheSerSerGlyProAspLeuGluProLeuIle							
AAGGAGATTGTCCGGCGCAATATCACGGGCAAGATCTGGCTGGCCAGCGAGGCCTGGGCCAGCTCTCCCTGATC							1350
LysGluIleValArgArgAsnIleThrGlyLysIleTrpLeuAlaSerGluAlaTrpAlaSerSerSerLeuIle							
GCCATGCCTCAGTACTTCCACGTGGTTGGCGGCACCATGGATTGCTCTGAAGGCTGGGCAGATCCCAGGCTTC							1425
AlaMetProGlnTyrPheHisValValGlyGlyThrIleGlyPheAlaLeuLysAlaGlyGlnIleProGlyPhe							
CGGAATTCTGAAGAAGGTCCATCCCAGGAAGTCTGTCCACAATGGTTTTGCCAAGGAGTTTTGGGAAGAAACA							1500
ArgGluPheLeuLysLysValHisProArgLysSerValHisAsnGlyPheAlaLysGluPheTrpGluGluThr							
TTTAAGTCCACCTCCAAGAAGGTGCAAAAGGACCTTTACCTGTGGACACCTTTCTGAGAGGTACCAAGAAAGT							1575
PheAsnCysHisLeuGlnGluGlyAlaLysGlyProLeuProValAspThrPheLeuArgGlyHisGluGluSer							

FIG. 48a.

10	20	30	40	50	60	70	
12345678901234567890123456789012345678901234567890123456789012345							
GCGCAGAGGTTTAGCAACAGCTCGACAGCCTTCGACCCCTCTGTACAGGGGATGAGAACATCAGCAGTGTGCGAG							1650
GlyAspArgPheSerAsnSerSerThrAlaPheArgProLeuCysThrGlyAspGluAsnIleSerSerValGlu							
ACCCCTTACATAGATTACACGCATTTACGGATATCCTACAATGTGTACTTAGCAGTCTACTCCATTGCCACGCC							1725
ThrProTyrIleAspTyrThrHisLeuArgIleSerTyrAsnValTyrLeuAlaValTyrSerIleAlaHisAla							
TTGCAAGATATATACCTGCTTACCTGGGAGAGGGCTCTTACCAATGGCTCCTGTGCAGACATCAAGAAAGTT							1800
LeuGlnAspIleTyrThrCysLeuProGlyArgGlyLeuPheThrAsnGlySerCysAlaAspIleLysLysVal							
GAGGCGTGGCAGGTCCTGAAGCACCTACGGCATCTAACTTTACAACAATATGGGGGAGCAGGTGACCTTTGAT							1875
GluAlaTrpGlnValLeuLysHisLeuArgHisLeuAsnPheThrAsnAsnMetGlyGluGlnValThrPheAsp							
GAGTGTGGTGACCTGGTGGGGAATTTCCATCATCACTGGCACCTCTCCCAGAGGATGGCTCCATCGTGT							1950
GluCysGlyAspLeuValGlyAsnTyrSerIleIleAsnTrpHisLeuSerProGluAspGlySerIleValPhe							
AAGGAAGTCGGGTATTACAACGTCTATGCCAAGAAGGGAGAAAGACTCTTCATCAACGAGGAGAAAAATCCTGTGG							2025
LysGluValGlyTyrTyrAsnValTyrAlaLysLysGlyGluArgLeuPheIleAsnGluGluLysIleLeuTrp							
AGTGGGTTCTCCAGGGAGCCACTCACCTTTGTGCTGTCTGTCTCCAGGTGCCCTTCTCCAACCTGCAGCCGAGAC							2100
SerGlyPheSerArgGluProLeuThrPheValLeuSerValLeuGlnValProPheSerAsnCysSerArgAsp							
TGCCTGGCAGGGACCCAGGAAAGGGATCATTGAGGGGGAGCCACCTGCTGCTTTGAGTGTGTGGAGTGTCTGAT							2175
CysLeuAlaGlyThrArgLysGlyIleIleGluGlyGluProThrCysCysPheGluCysValGluCysProAsp							
GGGGAGTATAGTGATGAGACAGATGCCAGTGCCTGTAACAAGTGCCAGATGACTTCTGGTCCAATGAGAACCAC							2250
GlyGluTyrSerAspGluThrAspAlaSerAlaCysAsnLysCysProAspAspPheTrpSerAsnGluAsnHis							
ACCTCTGCATTGCCAAGGAGATCGAGTTTCTGTCTGGACGGAGCCCTTTGGGATCGCACTCACCTCTTTGCC							2325
ThrSerCysIleAlaLysGluIleGluPheLeuSerTrpThrGluProPheGlyIleAlaLeuThrLeuPheAla							
GTGCTGGGCATTTTCTGACAGCCTTTGTGCTGGGTGTGTTTATCAAGTTCGCAACACCCATTGTCAAGGCC							2400
ValLeuGlyIlePheLeuThrAlaPheValLeuGlyValPheIleLysPheArgAsnThrProIleValLysAla							
ACCAACCGAGAGCTCTCTACCTCTCTCTTCTCCCTGCTGCTGCTTCTCCAGCTCCCTGTTCTTCATCGGG							2475
ThrAsnArgGluLeuSerTyrLeuLeuLeuPheSerLeuLeuCysCysPheSerSerSerLeuPhePheIleGly							
GAGCCCCAGGACTGGACGTGCCGCTGCGCCAGCCGGCCTTTGGCATCAGCTTCGTGCTCTGCATCTCATGCATC							2550
GluProGlnAspTrpThrCysArgLeuArgGlnProAlaPheGlyIleSerPheValLeuCysIleSerCysIle							
CTGGTGAAAACCAACCGTGCCTCCTGGTGTGAGGCCAAGATCCCCACCAGCTTCCACCGCAAGTGGTGGGGG							2625
LeuValLysThrAsnArgValLeuLeuValPheGluAlaLysIleProThrSerPheHisArgLysTrpTrpGly							
CTCAACCTGCAGTTCTGCTGGTTTTCTCTGCACCTTCATGCAGATTGTGATCTGTGTGATCTGGCTCTACACC							2700
LeuAsnLeuGlnPheLeuLeuValPheLeuCysThrPheMetGlnIleValIleCysValIleTrpLeuTyrThr							
GCGCCCCCTCAAGCTACCGCAACAGGAGCTGGAGGATGAGATCATCTTCATCAGTGCCACGAGGGCTCCCTC							2775
AlaProProSerSerTyrArgAsnGlnGluLeuGluAspGluIleIlePheIleThrCysHisGluGlySerLeu							
ATGGCCCTGGGCTTCTGATCGGCTACACCTGCCTGGCTGCCATCTGCTTCTTCTTTCGCTTCAAGTCCCGG							2850
MetAlaLeuGlyPheLeuIleGlyTyrThrCysLeuLeuAlaAlaIleCysPhePhePheAlaPheLysSerArg							
AAGTGCCGGAGAAGTTCAATGAAGCCAAGTTTCATCACCTTCAGCATGCTCATCTTCTTCATCGTCTGGATCTCC							2925
LysLeuProGluAsnPheAsnGluAlaLysPheIleThrPheSerMetLeuIlePhePheIleValTrpIleSer							
TTTATCCAGCCTATGCCAGCACCTATGGCAAGTTTGTCTCTGCCGTAGAGGTGATTGCCATCCTGGCAGCCAGC							3000
PheIleProAlaTyrAlaSerThrTyrGlyLysPheValSerAlaValGluValIleAlaIleLeuAlaAlaSer							
TTTGGCTTGTGGCGTGCATCTTCTTCAACAAGATCTACATCTTCTTCAAGCCATCCGCAACACCATCGAG							3075
PheGlyLeuLeuAlaCysIlePhePheAsnLysIleTyrIleIleLeuPheLysProSerArgAsnThrIleGlu							
GAGGTGCGTTGCAGCACCGCAGCTCACGCTTTCAAGGTGGCTGCCGGGCCACGCTGCCCGCAGCAACGTCTCC							3150
GluValArgCysSerThrAlaAlaHisAlaPheLysValAlaAlaArgAlaThrLeuArgSerAsnValSer							

FIG. 48b.

10	20	30	40	50	60	70	
12345678901234567890123456789012345678901234567890123456789012345							
CGCAAGCGGTCCAGCAGCCTTGGAGGCTCCACGGGATCCACCCCTCCTCCTCATCAGCAGCAAGAGCAACAGC							3225
ArgLysArgSerSerSerLeuGlyGlySerThrGlySerThrProSerSerSerIleSerSerLysSerAsnSer							
GAAGACCCATTCCACGGCCGAGAGGCAGAAGCAGCAGCAGCCGCTGGCCCTAACCCAGCAAGAGCAGCAGCAG							3300
GluAspProPheProArgProGluArgGlnLysGlnGlnGlnProLeuAlaLeuThrGlnGlnGluGlnGlnGln							
CAGCCCTGACCCCTCCACAGCAGCAACGATCTCAGCAGCAGCCAGATGCAAGCAGAAGGTCACTTTGGCAGC							3375
GlnProLeuThrLeuProGlnGlnGlnArgSerGlnGlnGlnProArgCysLysGlnLysValIlePheGlySer							
GGCAGGTACCTTTCTACTGAGCTTTGATGAGCCTCAGAAGAAGCCATGGCCACAGGAATTCTACGCACCAG							3450
GlyThrValThrPheSerLeuSerPheAspGluProGlnLysAsnAlaMetAlaHisArgAsnSerThrHisGln							
AACTCCCTGGAGGCCAGAAAAGCAGCGATACGCTGACCCGACACCGCCATTACTCCCGCTGCAGTGCAGGGGAA							3525
AsnSerLeuGluAlaGlnLysSerSerAspThrLeuThrArgHisGlnProLeuLeuProLeuGlnCysGlyGlu							
ACGGACTTAGATCTGACCGTCCAGGAACAGGTCTGCAAGGACCTGTGGGTGGAGACCAGCGCCAGAGGTGGAG							3600
ThrAspLeuAspLeuThrValGlnGluThrGlyLeuGlnGlyProValGlyGlyAspGlnArgProGluValGlu							
GACCTGAAGAGTTGTCCCCAGCACTTGTAGTGTCAGTTTCACAGAGCTTTGTATCAGTGGTGGAGGCAGCACT							3675
AspProGluGluLeuSerProAlaLeuValValSerSerSerGlnSerPheValIleSerGlyGlyGlySerThr							
GTTACAGAAAACGTAGTGAATTCATAAAATGGAAGGAGAAGACTGGGCTAGGGAGAATGCAGAGAGGTTTCTTGG							3750
ValThrGluAsnValValAsnSer...							
GGTCCCAGGGATGAGGAATCGCCCCAGACTCCTTTCTCTGAGGAAGAAGGGATAATAGACACATCAAATGCCCC							3825
GAATTTAGTCACACCATCTTAAATGACAGTGAATTGACCCATGTTCCCTTTAAATTAAGAGAGCCTT							3900
GTGTTTCTGTGGTTGCATTGTCAAGCATTGAGATCTCCACGGTCAGATTTGCTGTTACCCACATCTAATGTC							3975
TCTTCCTCTGTTCTATCCACCCAACAGCTCAGAGATGAACTATGGCTTTAACTACCTCCAGAGTGTGCAGA							4050
CTGATGGGACATCAAATTTGCCACCACTAGAGCTGAGAGTCTGAAAGACAGAATGTCACCAGTCTGCCCAATGC							4125
CTTGACAACAGACTGAATTTTAAATGTTCAACATAAGGAGAATGTATCTCCTCTATTTATGAAAACCATATG							4200
ATATTTTGTCTCCTACCTGCTGCTGCTATTATGTAACATCCAGAAGGTTTGACCCCTCCTATACCATATGTCTG							4275
GTTCTGTCCAGGACATGATACTGATGCCATGTTTAGATTCCAGGATCACAAGAATCACCTCAAATTGTTAGGAAG							4350
GGACTGCATAAACCAATGAGCTGTATCTGTAATTAATATTCCTATATGTAGCTTTATCCTTAGGAAAATGCTTCT							4425
GTTGTAATAGTCCATGGACAATATAAACTGAAAAATGTCAGTCTGGTTTATATAAGGCAGTATTATTGAGCTCTA							4500
TTTCCCCACCCCACTATCCTCACTCCCATAAGCTAAGCCTTATGTGAGCCCTTCAGGGACTCAAGGGTCCAGAA							4575
GTCCCTCCCATCTCTACCCCAAAGAATTCCTGAAGCCAGATCCACCTATCCCTGTACAGAGTAAGTTCTCAATT							4650
ATTGGCCTGCTAATAGCTGCTAGGGTAGGAAAGCGTGGTTCCAAGAAAGATCCACCCTCAAATGTCGGAGCTATG							4725

FIG. 48c.

[illegible]

Abstract

(Seq. I.D. No. 3)

[illegible]

FIG. 49a.

10	20	30	40	50	60	70	
12345678901234567890123456789012345678901234567890123456789012345							
AGCAGTGTGCGAGACCCCTTACATAGATTACACGCATTACGGATATCCTACAATGTGTACTTAGCAGTCTACTCC							1650
SerSerValGluThrProTyrIleAspTyrThrHisLeuArgIleSerTyrAsnValTyrLeuAlaValTyrSer							
ATTGCCACGCCTTGAAGATATATACCTGCTTACCTGGGAGAGGGCTCTTACCAATGGCTCCTGTGCAGAC							1725
IleAlaHisAlaLeuGlnAspIleTyrThrCysLeuProGlyArgGlyLeuPheThrAsnGlySerCysAlaAsp							
ATCAAGAAAGTTGAGGCGTGGCAGGTCTGAAGCACCTACGGCATCTAAACTTTACAAACAATATGGGGGAGCAG							1800
IleLysLysValGluAlaTrpGlnValLeuLysHisLeuArgHisLeuAsnPheThrAsnAsnMetGlyGluGln							
GTGACCTTTGATGAGTGTGGTACCTGGTGGGAACTATTCCATCATCAACTGGCACCTCTCCCCAGAGGATGGC							1875
ValThrPheAspGluCysGlyAspLeuValGlyAsnTyrSerIleIleAsnTrpHisLeuSerProGluAspGly							
TCCATCGTGTTTAAGGAAGTCGGGTATTACAACGCTATGCCAAGAAGGAGAAAGACTCTTCATCAACGAGGAG							1950
SerIleValPheLysGluValGlyTyrTyrAsnValTyrAlaLysLysGlyGluArgLeuPheIleAsnGluGlu							
AAAATCCTGTGGAGTGGGTCTCCAGGGAGGTGCCCTTCTCCAACGACGCGAGACTGCCTGGCAGGGACCAGG							2025
LysIleLeuTrpSerGlyPheSerArgGluValProPheSerAsnCysSerArgAspCysLeuAlaGlyThrArg							
AAAGGGATCATTGAGGGGAGCCACCTGCTGCTTTGAGTGTGTGGAGTGTCTGTATGGGGAGTATAGTGATGAG							2100
LysGlyIleIleGluGlyGluProThrCysCysPheGluCysValGluCysProAspGlyGluTyrSerAspGlu							
ACAGATGCCAGTGCCTGTAACAAGTGCCAGATGACTTCTGGTCCAATGAGAACCACACCTCCTGCATTGCCAAG							2175
ThrAspAlaSerAlaCysAsnLysCysProAspAspPheTrpSerAsnGluAsnHisThrSerCysIleAlaLys							
GAGATCGAGTTTCTGCTGGAGCGGAGCCCTTTGGGATCGCACTCACCTCTTTGCCGTGCTGGGCATTTTCTG							2250
GluIleGluPheLeuSerTrpThrGluProPheGlyIleAlaLeuThrLeuPheAlaValLeuGlyIlePheLeu							
ACAGCCTTTGTGCTGGGTGTGTTTATCAAGTTCCGCAACACACCCATTGTCAAGGCCACCAACCGAGAGCTCTCC							2325
ThrAlaPheValLeuGlyValPheIleLysPheArgAsnThrProIleValLysAlaThrAsnArgGluLeuSer							
TACCTCCTCCTCTTCTCCTGCTGCTGCTTCTCCAGCTCCCTGTTCTTCATCGGGGAGCCCCAGGACTGGAGC							2400
TyrLeuLeuLeuPheSerLeuLeuCysCysPheSerSerSerLeuPhePheIleGlyGluProGlnAspTrpThr							
TGCCGCTGCGCCAGCCGGCCTTTGGCATCAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG							2475
CysArgLeuArgGlnProAlaPheGlyIleSerPheValLeuCysIleSerCysIleLeuValLysThrAsnArg							
GTCCTCCTGGTGTGTTGAGGCCAAGATCCCCACAGCTTCCACCGCAAGTGGTGGGGGCTCAACCTGCAGTTCTCTG							2550
ValLeuLeuValPheGluAlaLysIleProThrSerPheHisArgLysTrpTrpGlyLeuAsnLeuGlnPheLeu							
CTGGTTTTCTCTGCACCTTCATGCAGATTGTCATCTGTGTGATCTGGCTCTACACCGCGCCCCCTCAAGCTAC							2625
LeuValPheLeuCysThrPheMetGlnIleValIleCysValIleTrpLeuTyrThrAlaProProSerSerTyr							
CGCAACCAGGAGCTGGAGGATGAGATCATCTTCATCAGTCCACGAGGGCTCCCTCATGGCCCTGGGCTTCCTG							2700
ArgAsnGlnGluLeuGluAspGluIleIlePheIleThrCysHisGluGlySerLeuMetAlaLeuGlyPheLeu							
ATCGGCTACACCTGCCTGCTGGCTGCCATCTGCTTCTTCTTTCGCTTCAAGTCCCGGAAGCTGCCGGAGAATTTC							2775
IleGlyTyrThrCysLeuLeuAlaAlaIleCysPhePhePheAlaPheLysSerArgLysLeuProGluAsnPhe							
AATGAAGCCAAGTTTCATCACCTTCAGCATGCTCATCTTCTTCATCGTCTGGATCTCCTTCATTCCAGCCTATGCC							2850
AsnGluAlaLysPheIleThrPheSerMetLeuIlePhePheIleValTrpIleSerPheIleProAlaTyrAla							
AGCACCTATGGCAAGTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG							2925
SerThrTyrGlyLysPheValSerAlaValGluValIleAlaIleLeuAlaAlaSerPheGlyLeuLeuAlaCys							
ATCTTCTCAACAAGATCTACATCTTCTTCAAGCCATCCCGCAACACCATCGAGGAGGTGCGTTGCAGCACC							3000
IlePhePheAsnLysIleTyrIleIleLeuPheLysProSerArgAsnThrIleGluGluValArgCysSerThr							
GCAGCTCACGCTTTCAAGGTGGCTGCCCGGCCACGCTGCGCCGCAACGCTCTCCGCAAGCGGTCCAGCAGC							3075
AlaAlaHisAlaPheLysValAlaAlaArgAlaThrLeuArgArgSerAsnValSerArgLysArgSerSerSer							
CTTGGAGGCTCCACGGGATCCACCCCTCTCTCTCATCAGCAGCAAGAGCAACAGCGAAGACCCATTCCACAG							3150
LeuGlyGlySerThrGlySerThrProSerSerSerIleSerSerLysSerAsnSerGluAspProPheProGln							

FIG. 49b.

pHuPCaR4.0 Sequence

10	20	30	40	50	60	70	
12345678901234567890123456789012345678901234567890123456789012345							
CCCGAGAGGCAGAAGCAGCAGCAGCCGCTGGCCCTAACCCAGCAAGAGCAGCAGCAGCCCTGACCCCTCCA							3225
ProGluArgGlnLysGlnGlnGlnProLeuAlaLeuThrGlnGlnGluGlnGlnGlnGlnProLeuThrLeuPro							
CAGCAGCAACGATCTCAGCAGCAGCCAGATGCAAGCAGAAGGTCATCTTTGGCAGCGGCACGGTCACCTTCTCA							3300
GlnGlnGlnArgSerGlnGlnGlnProArgCysLysGlnLysValIlePheGlySerGlyThrValThrPheSer							
CTGAGCTTTGATGAGCCTCAGAAGAACGCCATGGCCACGGGAATTCTACGCACCAGAACTCCCTGGAGGCCACG							3375
LeuSerPheAspGluProGlnLysAsnAlaMetAlaHisGlyAsnSerThrHisGlnAsnSerLeuGluAlaGln							
AAAAGCAGCGATACGCTGACCCGACACCAGCCATTAC[CCCGCTGCAGTGCGGGAAACGGACTTAGATCTGACC							3450
LysSerSerAspThrLeuThrArgHisGlnProLeuLeuProLeuGlnCysGlyGluThrAspLeuAspLeuThr							
GTCCAGGAAACAGGTCTGCAAGGACCTGTGGGTGGAGACCAGCGGCCAGAGGTGGAGGACCTGAAGAGTTGTCC							3525
ValGlnGluThrGlyLeuGlnGlyProValGlyGlyAspGlnArgProGluValGluAspProGluGluLeuSer							
CCAGCACTGTAGTGTCCAGTTCACAGAGCTTTGTCATCAGTGGTGGAGGCAGCACTGTTACAGAAAACGTAGTG							3600
ProAlaLeuValValSerSerSerGlnSerPheValIleSerGlyGlyGlySerThrValThrGluAsnValVal							
AATTCATAAAATGGAAGGAGAAGACTGGGCTAGGGAGAATGCAGAGAGGTTTCTTGGGGTCCCAGGGATGAGGAA							3675
AsnSer							
TCGCCCCAGACTCCTTTCTCTGAGGAAGAAGGGATAATAGACACATCAAATGCCCCGAATTTAGTCACACCATC							3750
TTAAATGACAGTGAATTGACCCATGTTCCCTTTAAAAAAAAAAAAAAAAAAGCGGCCGC							3809

FIG. 49c.

pRaKCaR Sequence
(Seq. I.D. No. 4)

10	20	30	40	50	60	70	
12345678901234567890123456789012345678901234567890123456789012345							
CGGGACTCTCCAGGCCGGCTCAGGCACCGGACTGTAGGTGTATTGGAGGGATTGGAGGCTGGAGACCCAGGA							75
AGCACGCAGGCGGGAGCAGGCAAGGGGCGGAGCCCCGGGCCCAAGGTGGCCGTCAGAGGGTCTGCGGGGAG							150
GCAGTAGCTTGACCCAAGGCGACCAAGGAACTTCAGACGGTAGCACGCCACTCAAACAAATTAACCTGACATCGC							225
AAGCTGGGCGGGCTGGTACGACATCCTGACTTCAGCATCCAGCTGTTCTTGGGCAGACAGAGGGCCAACAGGTGT							300
TCCTGTGGAAGAAGCCAGGACAAGGACTCCAGAAAACATCTCGGGCAGCCTCTACATGATGTCACTTCTCAGGAC							375
TCGAGGACCAGCCACCTTACACCTCTACTACAGAGAAGGCAGAAATGGAGACCCAAAGGCCATCACTCTCTCTCT							450
GTCCTAACCCTCTGTAAATCATGTCTCCCCACCAGAAGGTGTGAACCGCACCAGGGCGTGGAGTTCTCGGGCT							525
CCCAATCCACTGACACCTTTACCTGTCCCCTGAAGAGAAGGCAACGCTATGGCATCGTACAGCTGCTGTTGGCC							600
CTATTGGCTCTTGCTGGCACTCTCTGCCTATGGGCTGACCAGCGAGCCAAAAGAAGGGGACATTATCCTA							675
LeuLeuAlaLeuAlaTrpHisSerSerAlaTyrGlyProAspGlnArgAlaGlnLysLysGlyAspIleIleLeu							
GGAGGTCTCTTTCTATCCATTTTGGAGTAGCAGCCAAAGATCAAGATCTGAAGTCAAGACCAGAGTCTGTGGAG							750
GlyGlyLeuPheProIleHisPheGlyValAlaAlaLysAspGlnAspLeuLysSerArgProGluSerValGlu							
TGCATTAGGTATAACTTCCGTGGATTCCGATGGTTACAAGCCATGATATTGCCATAGAGGAGATAAACAGCAGC							825
CysIleArgTyrAsnPheArgGlyPheArgTrpLeuGlnAlaMetIlePheAlaIleGluGluIleAsnSerSer							
CCCTCCCTTCTTCCAACATGACACTGGGATATAGGATATTTGACACCTGTAACACCGTCTCCAAGCGCTGGAA							900
ProSerLeuLeuProAsnMetThrLeuGlyTyrArgIlePheAspThrCysAsnThrValSerLysAlaLeuGlu							
GCCACCTTGAAGTTTGTGGCCAGAACAAATCGATTCTTTGAACCTGGACGAGTTCTGCAACTGCTCTGAGCAC							975
AlaThrLeuSerPheValAlaGlnAsnLysIleAspSerLeuAsnLeuAspGluPheCysAsnCysSerGluHis							
ATCCCTTCGACCATTTGCCGTGGTGGGAGCCACCGGCTCCGGTGTCTCCACGGCGGTAGCCAACCTGCTGGGACTT							1050
IleProSerThrIleAlaValValGlyAlaThrGlySerGlyValSerThrAlaValAlaAsnLeuLeuGlyLeu							
TTCTACATCCCCAGGTGAGCTACGCCTCTCCAGCAGGCTCCTCAGCAATAAGAACCAGTACAAATCCTTCTCTC							1125
PheTyrIleProGlnValSerTyrAlaSerSerSerArgLeuLeuSerAsnLysAsnGlnTyrLysSerPheLeu							
CGCACCATCCCAATGACGAACACCAGGCAACCGGATGGCCGACATCATCGAGTACTTCCGCTGGAACCTGGGTG							1200
ArgThrIleProAsnAspGluHisGlnAlaThrAlaMetAlaAspIleIleGluTyrPheArgTrpAsnTrpVal							
GGCACAATTGCAGCTGATGACGACTATGGCAGACCTGGCATTGAGAAGTTCCGAGAGGAAGCCGAAGAGAGGGAT							1275
GlyThrIleAlaAlaAspAspAspTyrGlyArgProGlyIleGluLysPheArgGluGluAlaGluGluArgAsp							
ATCTGCATTGATTTAGCGAGCTCATCTCCAGTACTCTGACGAGGAAGAGATCCAGCAGGTGGTCAAGTGATC							1350
IleCysIleAspPheSerGluLeuIleSerGlnTyrSerAspGluGluGluIleGlnGlnValValGluValIle							
CAAACTCTACGGCCAAGGTCAATTGTCGTTTTCTCCAGCGGCCGGACCTAGAACCTCTCATCAAGGAGATTGTG							1425
GlnAsnSerThrAlaLysValIleValValPheSerSerGlyProAspLeuGluProLeuIleLysGluIleVal							
CGGCGTAACATCACAGGCAGGATCTGGCTGGCTAGCGAGGCTGGGCCAGTTTCTCGCTGATTGCTATGCCTGAG							1500
ArgArgAsnIleThrGlyArgIleTrpLeuAlaSerGluAlaTrpAlaSerSerSerLeuIleAlaMetProGlu							
TATTTCCATGTAGTCGGGGGCACCATTTGGGTTGGGCTGAAGGCTGGGCAGATTCCAGGCTTCAGAGAATTCCTA							1575
TyrPheHisValValGlyGlyThrIleGlyPheGlyLeuLysAlaGlyGlnIleProGlyPheArgGluPheLeu							

FIG. 50a.

pRaKCaR Sequence

10	20	30	40	50	60	70	
12345678901234567890123456789012345678901234567890123456789012345							
CAGAAAGTTCATCCTAGGAAGTCTGTCCACAATGGTTTTGCCAAAGAGTTTTGGGAAGAACTTTAATTGCCAC							1650
GlnLysValHisProArgLysSerValHisAsnGlyPheAlaLysGluPheTrpGluGluThrPheAsnCysHis							
CTCCAAGAAGGCGCAAAAGGACCTTTACCTGTGGACACCTTCGTGAGAAGTCACGAAGAAGGTGGCAACAGGTTA							1725
LeuGlnGluGlyAlaLysGlyProLeuProValAspThrPheValArgSerHisGluGluGlyGlyAsnArgLeu							
CTCAATAGCTCTACTGCCTTCGACCCCTCTGCACAGGGGATGAGAATCAACAGTGTGGAGACCCCTTACATG							1800
LeuAsnSerSerThrAlaPheArgProLeuCysThrGlyAspGluAsnIleAsnSerValGluThrProTyrMet							
GATTACGAACATTTACGGATATCCTACAATGTGTACTTAGCCGTCTACTCCATTGGCGATGCCCTACAAGATATA							1875
AspTyrGluHisLeuArgIleSerTyrAsnValTyrLeuAlaValTyrSerIleAlaHisAlaLeuGlnAspIle							
TACACCTGCTTACCCGGAAGAGGGCTTTTACCACAGGGTCTGTGCAGACATCAAGAAGGTTGAGGCCTGGCAG							1950
TyrThrCysLeuProGlyArgGlyLeuPheThrAsnGlySerCysAlaAspIleLysLysValGluAlaTrpGln							
GTCTTGAAGCACCTACGGCACCTGAACCTCACCAACAACATGGGGGAGCAGGTGACCTTCGATGAGTGTGGTGT							2025
ValLeuLysHisLeuArgHisLeuAsnPheThrAsnAsnMetGlyGluGlnValThrPheAspGluCysGlyAsp							
CTGGTGGGGAACCTATTCTATCATCAACTGGCACCTCTCCCGAGAGGACGGCTCCATTGTGTTCAAGGAAGTTGGG							2100
LeuValGlyAsnTyrSerIleIleAsnTrpHisLeuSerProGluAspGlySerIleValPheLysGluValGly							
TACTACAATGTGTATGCCAAGAAGGGAGAAAGACTCTTCATCAATGAGGAGAAGATCTTGTGGAGTGGGTTCTCC							2175
TyrTyrAsnValTyrAlaLysLysGlyGluArgLeuPheIleAsnGluGluLysIleLeuTrpSerGlyPheSer							
AGAGAGGTGCCTTTCTCCAATTGCAGCCGGGACTGTACGGCAGGGACCGAAGGGGATCATCGAGGGAGAGCCC							2250
ArgGluValProPheSerAsnCysSerArgAspCysGlnAlaGlyThrArgLysGlyIleIleGluGlyGluPro							
ACCTGCTGCTTTGAGTGTGTGGAGTGTCTGATGGAGAGTACAGTGGAGAGACAGATGCGAGTGCCTGTGACAAG							2325
ThrCysCysPheGluCysValGluCysProAspGlyGluTyrSerGlyGluThrAspAlaSerAlaCysAspLys							
TGCCCGGATGACTTCTGGTCCAATGAGAACCACACTTCTTGCAATGCCAAGGAGATTGAGTTTCTGGCGTGGACC							2400
CysProAspAspPheTrpSerAsnGluAsnHisThrSerCysIleAlaLysGluIleGluPheLeuAlaTrpThr							
GAGCCCTTTGGAATCGCTCTCACTCTCTTTGCGGTGCTGGGCATTTCTGACCGCCTTTGTGCTGGGTGCTTC							2475
GluProPheGlyIleAlaLeuThrLeuPheAlaValLeuGlyIlePheLeuThrAlaPheValLeuGlyValPhe							
ATCAAGTCCGAACACACCTATCGTCAAGGCCACCAACCGAGAAGTGTCTACCTCCTGCTCTTCTCCCTACTC							2550
IleLysPheArgAsnThrProIleValLysAlaThrAsnArgGluLeuSerTyrLeuLeuPheSerLeuLeu							
TGCTGCTTCTCCAGCTCCTTGTCTTCTATTGGGGAGCCCCAGGACTGGACGTGCCGCTGCGACAGCCTGCTTTC							2625
CysCysPheSerSerSerLeuPhePheIleGlyGluProGlnAspTrpThrCysArgLeuArgGlnProAlaPhe							
GGCATCAGCTTTGTGCTCTGTATCTCGTGCATCTTGGTGAAGACCAATCGCGTCTCTGGTATTTGAAGCCAAG							2700
GlyIleSerPheValLeuCysIleSerCysIleLeuValLysThrAsnArgValLeuLeuValPheGluAlaLys							
ATACCCACCAGCTTCCACCGAAGTGGTGGGGGCTCAACCTGCAGTTCCTGCTGGTTTTCTCTGCACCTTCATG							2775
IleProThrSerPheHisArgLysTrpTrpGlyLeuAsnLeuGlnPheLeuLeuValPheLeuCysThrPheMet							
CAGATCCTCATCTGCATCATCTGGCTCTACAGGCGCCCCCTCTAGCTACCGCAACCATGAGCTGGAAGACGAA							2850
GlnIleLeuIleCysIleIleTrpLeuTyrThrAlaProProSerSerTyrArgAsnHisGluLeuGluAspGlu							
ATCATCTTCATCAGTGCCATGAGGGCTCACTCATGGCACTTGGCTCCCTGATCGGCTATACCTGCCTGCTGGCT							2925
IleIlePheIleThrCysHisGluGlySerLeuMetAlaLeuGlySerLeuIleGlyTyrThrCysLeuLeuAla							
GCCATCTGCTTCTTCTTGGCTTCAAGTCCAGGAAGTTACCAGAGAAGTTCAACGAAGCCAAGTTACCTTC							3000
AlaIleCysPhePhePheAlaPheLysSerArgLysLeuProGluAsnPheAsnGluAlaLysPheIleThrPhe							
AGCATGCTCATCTTCTTCATCGTCTGGATCTCCTTCACTCCAGCCTATGCCAGCACCTACGGCAAGTTGTCTCT							3075
SerMetLeuIlePhePheIleValTrpIleSerPheIleProAlaTyrAlaSerThrTyrGlyLysPheValSer							
GCCGTAGAGGTGATCGCCATTTTGGCAGCCAGCTTTGGCTTACTAGCCTGCATCTTCTTCAACAAGGTCTACATT							3150
AlaValGluValIleAlaIleLeuAlaAlaSerPheGlyLeuLeuAlaCysIlePhePheAsnLysValTyrIle							

FIG. 50b.

12345678901234567890123456789012345678901234567890123456789012345

pRaKCaR Sequence

10	20	30	40	50	60	70	
12345678901234567890123456789012345678901234567890123456789012345							
ATCCTCTTCAAGCCTTCCCGGAACACCATTTGAGGAAGTCCGCTCCAGCACCAGCACATGCTTTCAAAGTAGCA							3225
IleLeuPheLysProSerArgAsnThrIleGluGluValArgSerSerThrAlaAlaHisAlaPheLysValAla							
GCCCGCGCCACTCTACGCCGTCCCAACATCTCCCGGAAGCGGTCCAGCAGCCTTGGAGGCTCCACCGGCTCCATT							3300
AlaArgAlaThrLeuArgArgProAsnIleSerArgLysArgSerSerSerLeuGlyGlySerThrGlySerIle							
CCCTCTCTCCATCAGCAGCAAAAGCAACAGCGAAGACCGGTTCCCGCAGCCAGAGAGGCAGAAGCAACAGCAA							3375
ProSerSerSerIleSerSerLysSerAsnSerGluAspArgPheProGlnProGluArgGlnLysGlnGlnGln							
CCGCTGTCTCCAGCCAGCAAGAACAGCAGCAGCAGCCCTGACCTCCACCCACAGCAACAGCAGCAGCCACAG							3450
ProLeuSerLeuThrGlnGlnGluGlnGlnGlnGlnProLeuThrLeuHisProGlnGlnGlnGlnGlnProGln							
CAGCCGAGATGCAAACAGAAGGTCTCTTCGGCAGTGGTACGGTCACCTTCTCTGAGTTTTGACGAGCCTCAG							3525
GlnProArgCysLysGlnLysValIlePheGlySerGlyThrValThrPheSerLeuSerPheAspGluProGln							
AAGAATGCCATGGCCACAGGAACCTCCATGCGTCAGAATCCCTGGAGGCCAGAGGAGCAACGACACCTTGGGC							3600
LysAsnAlaMetAlaHisArgAsnSerMetArgGlnAsnSerLeuGluAlaGlnArgSerAsnAspThrLeuGly							
AGACACCAGGCCCTGCTTCCCTACAGTGTGCAGATGCGGACTCAGAAATGACCATTACAGGAAACGGGCCTGCAA							3675
ArgHisGlnAlaLeuLeuProLeuGlnCysAlaAspAlaAspSerGluMetThrIleGlnGluThrGlyLeuGln							
GGGCCCATGGTGGGGGACCACCAGCCAGAAATGGAAGCTCAGATGAAATGTCCCAGCGCTGGTCTGTCCACC							3750
GlyProMetValGlyAspHisGlnProGluMetGluSerSerAspGluMetSerProAlaLeuValMetSerThr							
TCTCGGAGCTTCGTCTTAGTGGTGGAGGTAGCTCTGTGACGGAAAACGTATTACACTCTTAATGGAGGGAAAGG							3825
SerArgSerPheValIleSerGlyGlyGlySerSerValThrGluAsnValLeuHisSer							
CTATCCAGTTGAGAGGTTTTTCTTAGAGCCCTGAGCAAAAGGATGGGTCTTCTTTCTTCCAGGAAGCCAGGG							3900
AGAGTAGGTACGTCAAAGCCTGTACTCAGTTGCACTGCTTTGAATGACAGTGAAGTGAAGTGGTGTCTTTAGA							3975
GTAAAGAAGAGCCATGTTTTGGGGTCTTTTTCCAGAGCTCAGTATCACACCTGGGTTTGCTGAAGTCTTTTCC							4050
TCTGCTCTATCCACCATCAGTTCAGACGAAAGCAAGGCTCTAAGCTACCCATCTGCTTCCCTCAAAAAAAAAA							4125
AAAAAA							4131

FIG. 50c.

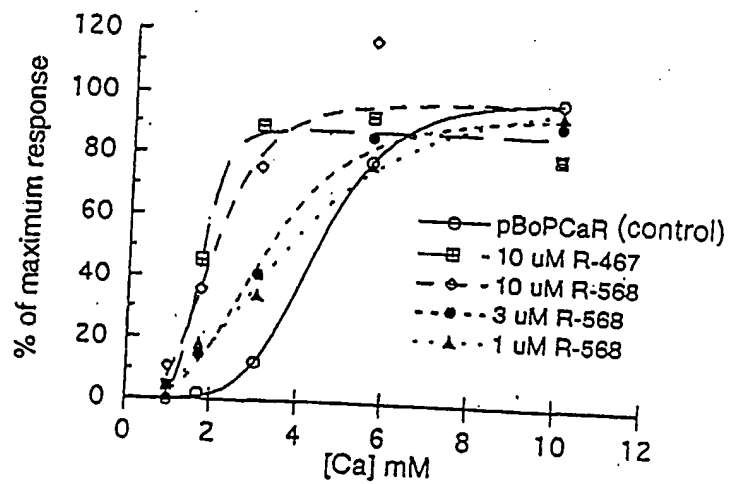


FIG. 51

Synthesis of 17X

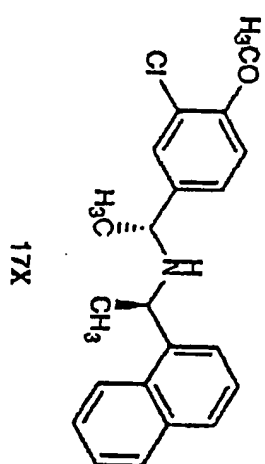
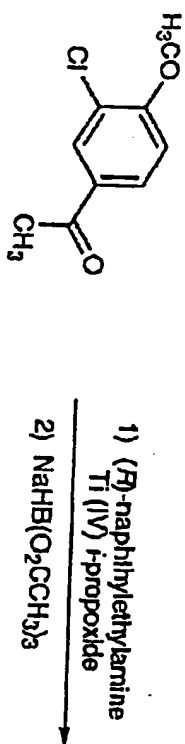
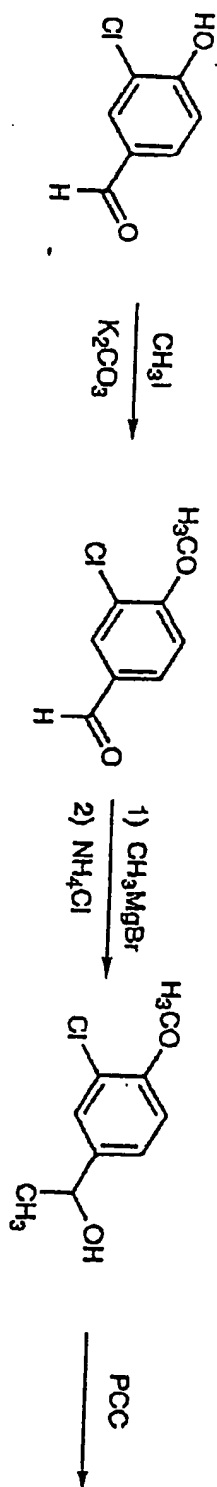


FIGURE 52